



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Renu Wadhwa et al.
Serial No. : 10/045,815
Filed : October 26, 2001
Title : TUMOR SUPPRESSOR GENE

Art Unit : 1642
Examiner : Misook Yu

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

TRANSMITTAL OF CERTIFIED TRANSLATION OF
PRIORITY DOCUMENT UNDER 35 USC §119

Applicant hereby submits an English language translation of priority document Japan Application No. 11/118806 filed April 26, 1999, together with a statement that the translation of the certified copy is accurate, in accordance with 35 USC § 119 and 37 CFR §1.55.

Please apply any charges or credits to Deposit Account No. 06-1050.

Respectfully submitted,

Date: 12/23/04

Janice L. Kugler REG. NO. 54,112
Reg. No. 50,429

Fish & Richardson P.C.
225 Franklin Street
Boston, MA 02110-2804
Telephone: (617) 542-5070
Facsimile: (617) 542-8906

20999504.doc

CERTIFICATE OF MAILING BY EXPRESS MAIL

Express Mail Label No. EV 411826827 US

December 23, 2004
Date of Deposit

VERIFICATION OF TRANSLATION

I, Mariko Ogura

of 6th Fl., Kantetsu Tsukuba-Science-City Bldg. 1-1-1, Oroshi-machi, Tsuchiura, Ibaraki,
JAPAN

declare as follows:

1. That I am well acquainted with both the English and Japanese languages, and
2. That the attached document is a true and correct translation made by me to the best of my knowledge and belief of:

Japanese Patent Application No. Hei 11-118806

Entitled: "Tumor Suppressor Gene"

Filed on April 26, 1999

November 19, 2004

(Date)

Mariko Ogura

(Signature of Translator)

Mariko Ogura

【Name of Document】 APPLICATION FOR PATENT

【Identification Number】 C1-104

【Filing Date】 April 26, 1999

【Addressee】 Esq. Commissioner of the Patent Office

【International Patent Classification】 C12N 15/12

【Inventor】

【Address】 c/o Chugai Research Institute for Medical Science, Inc.
153-2, Nagai, Niihari-mura, Niihari-gun, Ibaraki

【Name】 WADHWA, Renu

【Inventor】

【Address】 c/o Chugai Research Institute for Medical Science, Inc.
153-2, Nagai, Niihari-mura, Niihari-gun, Ibaraki

【Name】 SUGIHARA, Takashi

【Inventor】

【Address】 c/o Chugai Research Institute for Medical Science, Inc.
153-2, Nagai, Niihari-mura, Niihari-gun, Ibaraki

【Name】 YOSHIDA, Akiko

【Applicant】

【Identification Number】 596102791

【Name or Appellation】 Chugai Research Institute for Medical Science, Inc.

【Attorney】

【Identification Number】 100102978

【Patent Attorney】

【Name or Appellation】 Hatsushi Shimizu

【Nominated Attorney】

【Identification Number】 100108774

【Patent Attorney】

【Name or Appellation】 Kazunori Hashimoto

【Payment】

【Registration Number】 041092

【Amount】 21000

【List of Attached Documents】

【Name of Document】	Description	1
---------------------------	--------------------	----------

【Name of Document】	Drawings	1
---------------------------	-----------------	----------

【Name of Document】	Abstract	1
---------------------------	-----------------	----------

【Proof】 Necessary

[Document Name] DESCRIPTION

[Title of the Invention] TUMOR SUPPRESSOR GENE

[Claims]

[Claim 1] A protein consisting of an amino acid sequence of
5 SEQ ID NOs: 4 or 6, or a protein functionally equivalent to the protein
consisting of an amino acid sequence of SEQ ID NOs: 4 or 6, wherein
the protein comprising an amino acid sequence in which one or more
amino acids are replaced, deleted, inserted, and/or added.

10 [Claim 2] A protein functionally equivalent to the protein
consisting of an amino acid sequence of SEQ ID NOs: 4 or 6, wherein
the protein encoded by a DNA hybridizing with a DNA consisting of
a nucleotide sequence of SEQ ID NOs: 3 or 5, and encoding.

15 [Claim 3] A protein consisting of an amino acid sequence of
SEQ ID NOs: 2 or 8, or a protein functionally equivalent to the protein
consisting of an amino acid sequence of SEQ ID NOs: 2 or 8, wherein
the protein comprising an amino acid sequence in which one or more
amino acids are replaced, deleted, inserted, and/or added.

20 [Claim 4] A protein functionally equivalent to the protein
consisting of an amino acid sequence of SEQ ID NOs: 2 or 8, wherein
the protein encoded by a DNA hybridizing with a DNA consisting of
a nucleotide sequence of SEQ ID NOs: 1 or 7, and encoding.

[Claim 5] A DNA encoding the protein of any one of claims 1
to 4.

[Claim 6] A vector into which the DNA of claim 5 is inserted.

25 [Claim 7] A host cell harboring the vector of claim 6.

[Claim 8] A method for producing the protein of any one of claims
1 to 4, comprising the steps of culturing the host cell of claim 7.

[Claim 9] An antibody against the protein of any one of claims
1 to 4.

30 [Claim 10] A partial peptide of the protein of any one of claims
1 to 4.

[Claim 11] A DNA that specifically hybridizes with a DNA
consisting of a nucleotide sequence of SEQ ID NOs: 1, 3, 5, or 7 and
comprises at least 15 nucleotides.

35 [Claim 12] A method of screening for a compound that binds to
the protein of any one of claims 1 to 4, comprising the steps of:

- (a) contacting a subject sample, containing one or more test compounds, with the protein or the partial peptide thereof;
- (b) detecting the binding activity of the subject sample with the protein or the partial peptide thereof; and
- (c) selecting from the subject sample the compound having the ability to bind to the protein or the partial peptide thereof.

[Claim 13] A compound binding to the protein of any one of claims 1 to 4, which can be isolated by the method of claim 12.

[Claim 14] A method of screening for a compound that promotes or inhibits the activity of the protein of any one of claims 1 to 4, comprising the steps of:

- (d) culturing cells which express the protein or the partial peptide thereof in the presence of a subject sample containing one or more test compounds;
- (e) detecting the proliferation of the cell; and
- (f) selecting the compound which promotes or inhibits the proliferation of the cells as compared to the proliferation detected in the absence of the subject sample.

[Claim 15] A compound which promotes or inhibits the activity of the protein of any one of claims 1 to 4 and which can be isolated by the method of claim 14.

[Detailed Description of the Invention]

[0001]

[Technical Field of Industrial Application]

The present invention relates to the field of biological science, more specifically to the field of cancer research. In particular, the present invention relates to novel proteins involved in the proliferation mechanism of cells. The proteins of the present invention can be used, for example, as target molecules for developing drugs against cancer.

[0002]

[Prior Art]

From a cytogenetic and molecular biology perspective, there

appears to be a non-random mutation on human chromosome 1p in many malignant tumors (Caron, H. (1995) *Med Pediatr Oncol* 24, 215-21; Schwab M. et al (1996) *Genes Chromosomes Cancer* 16, 211-29). For example, deletions in the region of chromosome 1p have been found in various oncocytes (neuroblastomas [White, P. S. et al (1997) *Eur J Cancer* 33, 1957-61, Gros16; Ariyama T. et al (1995) *Genomics* 25, 114-23; Cheng, N. C. et al (1995) *Oncogene* 10, 291-7], meningiomas [Ishino, S. et al (1998) *Cancer* 83, 360-6], pheochromocytomas, medullary thyroid carcinomas, neuroendocrine tumors [Moley, J. F. et al (1992) *Cancer Res* 52, 770-4], T cell acute lymphoblastic leukemia (T-ALL) [Iolascon, A. et al (1997) *Leukemia* 11, 359-63], colorectal cancers [Praml, C. et al (1995) *Oncogene* 11, 1357-62, Gros13; Bomme, L. et al (1998) *Genes Chromosomes Cancer* 21, 185-94; Di Vinci, A. et al (1998) *Cancer* 83, 415-22], mesotheliomas [Lee, W. C. et al (1996) *Cancer Res* 56, 4297-301], hepatomas [Chen, H. L. et al (1996) *Cancer Genet Cytogenet* 86, 102-6], endometrial carcinomas [Arlt, M. F. et al (1996) *Hum Mol Genet* 5, 1017-21], and breast cancers [Nagai, H. et al (1995) *Cancer Res* 55, 1752-7; Munn, K. E. et al (1995) *Oncogene* 10, 1653-7]. etc.). In addition, mutations in the 1p region are thought to correlate with lymph node metastasis and tumor size [Borg, A. et al (1992) *Genes Chromosomes Cancer* 5, 311-20; Tsukamoto, K. et al (1998) *Cancer* 82, 317-22]. Moreover, the genetic mutation associated with endodermal sinus tumors (CESTs) developed in small children under four years is proposed to occur on chromosome 1p [Perlman, E. J. et al (1996) *Genes Chromosomes Cancer* 16, 15-20]. These facts indicate that one or more genetic mutations in chromosome 1p are associated with malignant tumors. However, the causative gene has not yet been discovered.

[0003]

[Problems to Be Solved by the Invention]

The object of the present invention is to provide a novel protein involved in the proliferation mechanism of the cells and the gene encoding the protein, as well as methods for producing and using the same.

[0004]

[Means to Solve the Problems]

The present inventors screened the mouse RS-4 cell cDNA library according to the immunoscreening method using antibodies against protein p33, which is about 30kDa in size and contained in the Triton X-100 insoluble fraction of the immortalized cell (NIH3T3) plasma membrane P100 fraction . Using thus obtained cDNA as a probe, human testis library was screened and the inventors succeeded in cloning the novel gene, Gros1, from the library. Two types of human Gros1 cDNAs (SEQ ID NOs: 1 and 3) exist: one encodes a protein consisting of 363 amino acids (designated "human Gros1-S protein", SEQ ID NO: 2), and the other encodes a protein consisting of 736 amino acids (designated "human Gros1-L protein", SEQ ID NO: 4).

[0005]

Moreover, using the cDNAs obtained by the above immunoscreening method as a probe, mouse testis library was both screened and searched for ESTs, to successfully identify mouse Gros1-L cDNA (SEQ ID NO: 5) and mouse Gros1-S cDNA (SEQ ID NO: 7). They encode a protein consisting of 747 amino acids (SEQ ID NO: 6) and 542 amino acids (SEQ ID NO: 8), respectively.

[0006]

Nothing was found to be significantly corresponded to Human and mouse Gros1s in the protein database. However, as a result of the motif search analysis of amino acid sequences, the amino acid sequences of mouse and human Gros1-Ls were found to comprise the leucine zipper structure often observed in some members of the transcription factors.

[0007]

As the result of chromosome mapping of human Gros1, the Gros1 gene was found to exist on the human chromosome 1 short arm (1p), a site suggested to have non-random mutations in many malignant tumors (Caron, H. (1995) Med Pediatr Oncol 24, 215-21; Schwab, M. et al (1996) Genes Chromosomes Cancer 16, 211-29).

[0008]

The amount of Gros1 mRNA expressed in tissues, cells and those during developmental stages was detected by Northern blot analysis. As a result, in human, 4.4 kb and 2.5 kb bands were strongly expressed in testis, ovary and placenta, and weakly in most other tissues (Figure

4). In addition, mRNA expression was higher in cultured human cells than in above tissues, and, in human normal cultured cells, the expression of the 2.5 kb mRNA was almost 10 times higher than that for the 4.4 kb mRNA (Figure 5). In mouse, 3.5 kb and 2.5 kb bands
5 were weakly expressed in most tissues, not expressed in brain or spleen; only the 2.5 kb band was expressed in the testis. Accordingly, in the testis and ovary, only the shorter form among the two transcripts of the Gros1 genes was detected. The expression during the developmental process was shown to dramatically disappear on the
10 11th day of the developmental process (Figure 6).

[0009]

The present inventors performed a function analysis of Gros1 by introducing the gene encoding the mouse 85 kDa protein (Gros1-L; SEQ ID NO: 6) into NIH3T3 cells. As a result, cell proliferation was
15 repressed and colony forming activity was decreased in cells expressing the full-length Gros1-L as compared to those of the control and Gros1 whose C-terminus is deleted. On the other hand, in cells in which antisense RNA of Gros1-L was expressed, the colony forming activity increased 5 folds.

20 [0010]

Based on these analyses, Gros1 proteins are thought to be novel genes involved in the control of cell proliferation, and related to the development and growth of tumors. Thus, Gros1 proteins are useful as tools for developing pharmaceuticals against tumors.

25 [0011]

The present invention relates to novel proteins (Gros1) involved in cell proliferation and the genes encoding them, as well as the production and the use the same. More specifically, the present invention provides the following:

30 (1) a protein consisting of an amino acid sequence of SEQ ID NOs: 4 or 6, or a protein functionally equivalent to the protein consisting of an amino acid sequence of SEQ ID NOs: 4 or 6, wherein the protein comprising an amino acid sequence in which one or more amino acids are replaced, deleted, inserted, and/or added;

35 (2) a protein functionally equivalent to the protein consisting of an amino acid sequence of SEQ ID NOs: 4 or 6, wherein the protein

encoded by a DNA hybridizing with a DNA consisting of a nucleotide sequence of SEQ ID NOs: 3 or 5, and encoding;

(3) a protein consisting of an amino acid sequence of SEQ ID NOs: 2 or 8, or a protein functionally equivalent to the protein consisting of an amino acid sequence of SEQ ID NOs: 2 or 8, wherein the protein comprising an amino acid sequence in which one or more amino acids are replaced, deleted, inserted, and/or added;

(4) a protein functionally equivalent to the protein consisting of an amino acid sequence of SEQ ID NOs: 2 or 8, wherein the protein encoded by a DNA hybridizing with a DNA consisting of a nucleotide sequence of SEQ ID NOs: 1 or 7, and encoding;

(5) a DNA encoding the protein of any one of (1) to (4);

(6) a vector into which the DNA of (5) is inserted;

(7) a host cell harboring the vector of (6);

(8) a method for producing the protein of any one of (1) to (4), comprising the steps of culturing the host cell of (7);

(9) an antibody against the protein of any one of (1) to (4);

(10) a partial peptide of the protein of any one of (1) to (4);

(11) a DNA that specifically hybridizes with a DNA consisting of a nucleotide sequence of SEQ ID NOs: 1, 3, 5, or 7 and comprises at least 15 nucleotides;

(12) a method of screening for a compound that binds to the protein of any one of (1) to (4), comprising the steps of:

(g) contacting a subject sample, containing one or more test compounds, with the protein or the partial peptide thereof;

(h) detecting the binding activity of the subject sample with the protein or the partial peptide thereof; and

(i) selecting from the subject sample the compound having the ability to bind to the protein or the partial peptide thereof;

(13) a compound binding to the protein of any one of (1) to (4), which can be isolated by the method of (12);

(14) a method of screening for a compound that promotes or inhibits the activity of the protein of any one of (1) to (4), comprising the steps of:

(j) culturing cells which express the protein or the partial peptide thereof in the presence of a subject sample containing one or more test compounds;

(k) detecting the proliferation of the cell; and

5 (l) selecting the compound which promotes or inhibits the proliferation of the cells as compared to the proliferation detected in the absence of the subject sample;

10 (15) a compound which promotes or inhibits the activity of the protein of any one of (1) to (4) and which can be isolated by the method of (14).

[0012]

[Mode for Carrying Out the Invention]

15 The present invention relates to a novel protein Gros1 involved in the cell proliferation mechanism. SEQ ID NOs: 1 and 3 show nucleotide sequences of the cDNA of two types of human Gros1 (human Gros1-S and human Gros1-L, respectively) isolated by the inventors, and SEQ ID NOs: 2 and 4 show the amino acids sequences encoded by the cDNAs, respectively. SEQ ID NOs: 5 and 7 show nucleotide sequences
20 of the cDNA of two types of mouse Gros1 (mouse Gros1-L and mouse Gros1-S, respectively) isolated by the present inventors, and SEQ ID NOs: 6 and 8 show the amino acids sequences encoded by the cDNAs, respectively.

[0013]

25 When the Gros1-L protein was expressed exogenously in NIH-3T3 cells, cell proliferation was inhibited and the colony forming activity decreased. In contrast, when the expression of Gros1-L protein was repressed by the introduction of Gros1 antisense cDNA in NIH-3T3 cells, the colony forming activity increased dramatically.
30 Thus, the Gros1 protein is considered to be involved in the control of cell proliferation. This is also supported by the fact that human Gros1 gene is present on chromosome 1 short arm (1p), a site that is purportedly associated with malignant tumors. Therefore, the Gros1 proteins of the present invention can be conveniently used as
35 tools, for purifying or cloning factors controlling cell proliferation, as well as targets, for example, for screening

candidate compounds of drugs useful for treating or preventing disorders related to cell proliferation, such as tumors. Moreover, the Gros1 genes can be applied in the treatment, for example, gene therapy for various tumors.

5 [0014]

The present invention encompasses proteins functionally equivalent to the Gros1 proteins. Such proteins include, for example, homologous proteins of other organisms corresponding to the human or mouse Gros1 protein, as well as mutants of human or mouse Gros1 proteins.

10 [0015]

In the present invention, the term "functionally equivalent" means that the subject protein has the activity to inhibit cell proliferation like Gros1 proteins. Whether the subject protein has a cell proliferation inhibitory activity or not can be judged by introducing the DNA encoding the subject protein into a cell, such as NIH-3T3, expressing the protein, and detecting repression of proliferation of the cells or reduction in colony forming activity.

[0016]

20 Methods for preparing proteins functionally equivalent to a given protein are well known by a person skilled in the art and include known methods of introducing mutations into the protein. For example, one skilled in the art can prepare proteins functionally equivalent to the human or mouse Gros1 protein by introducing an appropriate mutation in the amino acid sequence of the human or mouse Gros1 protein by site-directed mutagenesis (Hashimoto-Gotoh, T. et al. (1995), Gene 152, 271-275; Zoller, MJ, and Smith, M. (1983), Methods Enzymol. 100, 468-500; Kramer, W. et al. (1984), Nucleic Acids Res. 12, 9441-9456; Kramer W, and Fritz HJ. (1987) Methods. Enzymol. 154, 350-367; Kunkel, TA (1985), Proc. Natl. Acad. Sci. USA. 82, 488-492; Kunkel (1988), Methods Enzymol. 85, 2763-2766). Amino acid mutations can occur in nature, too. The protein of the present invention includes those proteins having the amino acid sequences of the human or mouse Gros1 protein in which one or more amino acids are mutated, provided the resulting mutated proteins are functionally equivalent to the human or mouse Gros1 protein. The number of amino acids to be mutated in

such a mutant is generally 10 amino acids or less, preferably 6 amino acids or less, and more preferably 3 amino acids or less.

[0017]

5 Mutated or modified proteins, proteins having amino acid sequences modified by deleting, adding and/or replacing one or more amino acid residues of a certain amino acid sequence, have been known to retain the original biological activity (Mark, D. F. et al., Proc. Natl. Acad. Sci. USA (1984) 81, 5662-5666, Zoller, M. J. & Smith, M., Nucleic Acids Research (1982) 10, 6487-6500, Wang, A. et al.,
10 Science 224, 1431-1433, Dalbadie-McFarland, G. et al., Proc. Natl. Acad. Sci. USA (1982) 79, 6409-6413).

[0018]

The amino acid residue to be mutated is preferably mutated into a different amino acid in which the properties of the amino acid
15 side-chain are conserved. Examples of properties of amino acid side chains are hydrophobic amino acids (A, I, L, M, F, P, W, Y, V), hydrophilic amino acids (R, D, N, C, E, Q, G, H, K, S, T), and side chains having the following functional groups or characteristics in common: an aliphatic side-chain (G, A, V, L, I, P); a hydroxyl group
20 containing side-chain (S, T, Y); a sulfur atom containing side-chain (C, M); a carboxylic acid and amide containing side-chain (D, N, E, Q); a base containing side-chain (R, K, H); and an aromatic containing side-chain (H, F, Y, W) (The parenthetic letters indicate the one-letter codes of amino acids).

25 [0019]

An example of a protein to which one or more amino acids residues are added to the amino acid sequence of human or mouse Gros1 protein (SEQ ID NOs: 2, 4, 6, or 8) is a fusion protein containing the human or mouse Gros1 protein. Fusion proteins are, fusions of the human
30 or mouse Gros1 protein and other peptides or proteins, and are included in the present invention. Fusion proteins can be made by techniques well known to a person skilled in the art, such as by linking the DNA encoding the human or mouse Gros1 protein of the invention with DNA encoding other peptides or proteins, so that the frames match,
35 inserting the fusion DNA into an expression vector and expressing it in a host. There is no restriction as to the peptides or proteins

fused to the protein of the present invention.

[0020]

Known peptides that can be used as peptides that are fused to the protein of the present invention include, for example, FLAG (Hopp, T. P. et al., Biotechnology (1988) 6, 1204-1210), 6xHis containing six His (histidine) residues, 10xHis, HA (Influenza agglutinin), human c-myc fragment, VSP-GP fragment, p18HIV fragment, T7-tag, HSV-tag, E-tag, SV40T antigen fragment, lck tag, α -tubulin fragment, B-tag, Protein C fragment, and the like. Examples of proteins that may be fused to a protein of the invention include GST (glutathione-S-transferase), HA (Influenza agglutinin), immunoglobulin constant region, β -galactosidase, MBP (maltose-binding protein), and such.

[0021]

Fusion proteins can be prepared by fusing commercially available DNA, encoding the fusion peptides or proteins discussed above, with the DNA encoding the protein of the present invention and expressing the fused DNA prepared.

[0022]

An alternative method known in the art to isolate functionally equivalent proteins is, for example, the method using a hybridization technique (Sambrook, J. et al., Molecular Cloning 2nd ed. 9.47-9.58, Cold Spring Harbor Lab. Press, 1989). One skilled in the art can readily isolate a DNA having high homology with a whole or part of the DNA sequence (SEQ ID NOs: 1, 3, 5 or 7) encoding the human or mouse Gros1 protein, and isolate functionally equivalent proteins to the human or mouse Gros1 protein from the isolated DNA. The proteins of the present invention include those that are encoded by DNA that hybridize with a whole or part of the DNA sequence encoding the human or mouse Gros1 protein and are functionally equivalent to the human or mouse Gros1 protein. These proteins include mammal homologues corresponding to the protein derived from human or mouse (for example, a protein encoded by a monkey, rat, rabbit and bovine gene). In isolating a cDNA highly homologous to the DNA encoding the human or mouse Gros1 protein from animals, it is particularly preferable to use tissues from ovary or testis.

[0023]

The condition of hybridization for isolating a DNA encoding a protein functionally equivalent to the human or mouse Gros1 protein can be routinely selected by a person skilled in the art. For example, hybridization may be performed by conducting prehybridization at 68°C for 30 min or longer using "Rapid-hyb buffer" (Amersham LIFE SCIENCE), adding a labeled probe, and warming at 68°C for 1 hour or longer. The following washing step can be conducted, for example, in a low stringent condition. A low stringent condition is, for example, 42°C, 2X SSC, 0.1% SDS, or preferably 50°C, 2X SSC, 0.1% SDS. More preferably, high stringent conditions are used. A high stringent condition is, for example, washing 3 times in 2X SSC, 0.01% SDS at room temperature for 20 min, then washing 3 times in 1x SSC, 0.1% SDS at 37°C for 20 min, and washing twice in 1x SSC, 0.1% SDS at 50°C for 20 min. However, several factors such as temperature and salt concentration can influence the stringency of hybridization and one skilled in the art can suitably select the factors to achieve the requisite stringency.

[0024]

In place of hybridization, a gene amplification method, for example, the polymerase chain reaction (PCR) method, can be utilized to isolate a DNA encoding a protein functionally equivalent to the human or mouse Gros1 protein, using a primer synthesized based on the sequence information of the DNA (SEQ ID NO: 1, 3, 5 or 7) encoding the human or mouse Gros1 protein.

[0025]

Proteins that are functionally equivalent to the human or mouse Gros1 protein encoded by the DNA isolated through the above hybridization techniques or gene amplification techniques, normally have a high homology to the amino acid sequence of the human or mouse Gros1 protein. "High homology" typically refers to a homology of 40% or higher, preferably 60% or higher, more preferably 80% or higher, even more preferably 95% or higher. The homology of a protein can be determined by following the algorithm in "Wilbur, W. J. and Lipman, D. J. Proc. Natl. Acad. Sci. USA (1983) 80, 726-730".

[0026]

A protein of the present invention may have variations in amino

acid sequence, molecular weight, isoelectric point, the presence or absence of sugar chains, or form, depending on the cell or host used to produce it or the purification method utilized. Nevertheless, so long as it has a function equivalent to that of the human or mouse
5 Gros1 protein (SEQ ID NO: 2, 4, 6 or 8) of the present invention, it is within the scope of the present invention.

[0027]

The proteins of the present invention can be prepared as recombinant proteins or natural proteins, by methods well known to
10 those skilled in the art. A recombinant protein can be prepared by inserting a DNA, which encodes the protein of the present invention (for example, the DNA comprising the nucleotide sequence of SEQ ID NOs: 1, 3, 5, or 7), into an appropriate expression vector, introducing the vector into an appropriate host cell, collecting thus obtained
15 recombinants, obtaining the extract thereof, and purifying the protein by subjecting the extract to chromatography, for example, ion exchange chromatography, reverse phase chromatography, gel filtration, or affinity chromatography utilizing a column to which antibodies against the protein of the present invention is fixed,
20 or by combining more than one of aforementioned columns.

[0028]

Also when the protein of the present invention is expressed within host cells (for example, animal cells and *E. coli*) as a fusion protein with glutathione-S-transferase protein or as a recombinant
25 protein supplemented with multiple histidines, the expressed recombinant protein can be purified using a glutathione column or nickel column.

[0029]

After purifying the fusion protein, it is also possible to
30 exclude regions other than the objective protein by cutting with thrombin or factor-Xa as required.

[0030]

A natural protein can be isolated by methods known to a person skilled in the art, for example, by contacting the affinity column,
35 in which antibodies binding to the Gros1 protein described below are bound, with the extract of tissues or cells expressing the protein

of the present invention. The antibodies can be polyclonal antibodies or a monoclonal antibodies.

[0031]

The present invention also encompasses partial peptides of the protein of the present invention. The partial peptide has an amino acid sequence specific to the protein of the present invention and consists of at least 7 amino acids, preferably 8 amino acids or more, and more preferably 9 amino acids or more. The partial peptide can be used, for example, for preparing antibodies against the protein of the present invention, screening for a compound that binds to the protein of the present invention, and screening for accelerators or inhibitors of the protein of the present invention.

[0032]

A partial peptide of the invention can be produced by genetic engineering, by known methods of peptide synthesis, or by digesting the protein of the invention with an appropriate peptidase. For peptide synthesis, for example, solid phase synthesis or liquid phase synthesis may be used.

[0033]

Furthermore, the present invention relates to DNA encoding the proteins of the present invention. The DNA of the present invention can be used for the *in vivo* or *in vitro* production of the protein of the present invention as described above, or can be applied to gene therapy for diseases attributed to genetic abnormality in the gene encoding the protein of the present invention. Any form of the DNA of the present invention can be used, so long as it encodes the protein of the present invention. Specifically, cDNA synthesized from the mRNA, genomic DNA, and chemically synthesized DNA can be used. The DNA of the present invention include a DNA comprising a given nucleotide sequences as well as its degenerate sequences, so long as the resulting DNA encodes a protein of the present invention.

[0034]

The DNA of the present invention can be prepared by methods known to a person skilled in the art. For example, the DNA of the present invention can be prepared by: preparing a cDNA library from cells which express the protein of the present invention, and

conducting hybridization using a partial sequence of the DNA of the present invention (for example, SEQ ID NOs: 1, 3, 5, or 7) as a probe. A cDNA library can be prepared, for example, by the method described in Sambrook J. et al., Molecular Cloning, Cold Spring Harbor Laboratory Press (1989); alternatively, commercially available cDNA libraries may be used. A cDNA library can be also prepared by: extracting RNAs from cells expressing the protein of the present invention, synthesizing oligo DNAs based on the sequence of the DNA of the present invention (for example, SEQ ID NOs: 1, 3, 5 or 7), conducting PCR by using the oligos as primers, and amplifying cDNAs encoding the protein of the present invention.

[0035]

In addition, by sequencing the nucleotides of the obtained cDNA, the translation region encoded by the cDNA can be determined, and the amino acid sequence of the protein of the present invention can be obtained. Moreover, by screening the genomic DNA library using the obtained cDNA as a probe, the genomic DNA can be isolated.

[0036]

More specifically, mRNAs may first be prepared from cells, tissue, or organ (for example, ovary, testis, placenta, etc.) in which the protein of the invention is expressed. Known methods can be used to isolate mRNAs; for instance, total RNA may be prepared by guanidine ultracentrifugation (Chirgwin J. M. et al. Biochemistry 18:5294-5299 (1979)) or AGPC method (Chomczynski P. and Sacchi N. Anal. Biochem. 162:156-159 (1987)). In addition, mRNA may be purified from total RNA using mRNA Purification Kit (Pharmacia) and such or, alternatively, mRNA may be directly purified by QuickPrep mRNA Purification Kit (Pharmacia).

[0037]

The obtained mRNA is used to synthesize cDNA using reverse transcriptase. cDNA may be synthesized by using a commercially available kit, such as the AMV Reverse Transcriptase First-strand cDNA Synthesis Kit (Seikagaku Kogyo). Alternatively, cDNA may be synthesized and amplified following the 5'-RACE method (Frohman M. A. et al. Proc. Natl. Acad. Sci. U.S.A. 85:8998-9002 (1988); Belyavsky A. et al. Nucleic Acids Res. 17:2919-2932 (1989)), which uses a primer

and such, described herein, the 5'-Ampli FINDER RACE Kit (Clontech), and polymerase chain reaction (PCR).

[0038]

A desired DNA fragment is prepared from the PCR products and
5 ligated with a vector DNA. The recombinant vectors are used to transform *E. coli* and such, and a desired recombinant vector is prepared from a selected colony. The nucleotide sequence of the desired DNA can be verified by conventional methods, such as dideoxynucleotide chain termination.

10 [0039]

The nucleotide sequence of a DNA of the invention may be designed to be expressed more efficiently by taking into account the frequency of codon usage in the host to be used for expression (Grantham R. et al. Nucleic Acids Res. 9:43-74 (1981)). The DNA of
15 the present invention may be altered by a commercially available kit or a conventional method. For instance, the DNA may be altered by digestion with restriction enzymes, insertion of a synthetic oligonucleotide or an appropriate DNA fragment, addition of a linker, or insertion of the initiation codon (ATG) and/or the stop codon (TAA,
20 TGA, or TAG).

[0040]

Specifically, the DNA of the present invention encompasses the DNA comprising the nucleotide sequence from base A at position 52 to base C at position 1140 of SEQ ID No: 1; the DNA from base A
25 at position 52 to base A at position 2259 of SEQ ID No: 3; the DNA from base A at position 12 to base G at position 2252 of SEQ ID No: 5; and that from base A at position 12 to base A at position 1640 of SEQ ID No: 3.

[0041]

30 Furthermore, the present invention provides a DNA that hybridizes under stringent conditions with a DNA having a nucleotide sequence of SEQ ID NOs: 1, 3, 5 or 7, and encodes a protein functionally equivalent to the protein of the invention described above.

[0042]

35 One skilled in the art may appropriately choose stringent conditions. For example, low stringent condition can be used. More

preferably, high stringent condition can be used. These conditions are the same as those described above. The hybridizing DNA above is preferably a cDNA or a chromosomal DNA.

[0043]

5 The present invention also relates to a vector into which a DNA of the present invention is inserted. A vector of the present invention is useful to keep a DNA of the present invention in host cell, or to express the protein of the present invention.

[0044]

10 When *E. coli* is a host cell and the vector is amplified and produced in a large amount in *E. coli* (e.g., JM109, DH5 α , HB101, or XL1Blue), the vector should have "ori" to be amplified in *E. coli* and a marker gene for selecting transformed *E. coli* (e.g., a drug-resistance gene selected by a drug such as ampicillin, tetracycline, kanamycin, chloramphenicol or the like). For example, 15 M13-series vectors, pUC-series vectors, pBR322, pBluescript, pCR-Script, etc. can be used. In addition, pGEM-T, pDIRECT, and pT7 can also be used for subcloning and extracting cDNA as well as the vectors described above. When a vector is used to produce the protein of the present invention, an expression vector is especially useful. For example, an expression vector to be expressed in *E. coli* should have the above characteristics to be amplified in *E. coli*. When *E. coli*, such as JM109, DH5 α , HB101, or XL1 Blue, are used as a host cell, the vector should have a promoter, for example, lacZ promoter 25 (Ward et al., Nature (1989) 341, 544-546; FASEB J (1992) 6, 2422-2427), araB promoter (Better et al., Science (1988) 240, 1041-1043), or T7 promoter or the like, that can efficiently express the desired gene in *E. coli*. In that respect, pGEX-5X-1 (Pharmacia), "QIAexpress system" (Qiagen), pEGFP and pET (in this case, the host is preferably BL21 which expresses T7 RNA polymerase), for example, can be used 30 instead of the above vectors.

[0045]

Additionally, the vector may also contain a signal sequence for polypeptide secretion. An exemplary signal sequence that directs 35 the protein to be secreted to the periplasm of the *E. coli* is the pelB signal sequence (Lei, S. P. et al J. Bacteriol. (1987) 169, 4379).

Means for introducing the vectors into the target host cells include, for example, the calcium chloride method, and the electroporation method.

[0046]

5 In addition to *E. coli*, for example, expression vectors derived from mammals (for example, pcDNA3 (Invitrogen) and pEGF-BOS (Nucleic Acids. Res. 1990, 18 (17), p5322), pEF, pCDM8), expression vectors derived from insect cells (for example, "Bac-to-BAC baculovirus expression system" (GIBCO BRL), pBacPAK8), expression vectors derived
10 from plants (for example pMH1, pMH2), expression vectors derived from animal viruses (for example, pHSV, pMV, pAdexLcw), expression vectors derived from retroviruses (for example, pZIpneo), expression vector derived from yeast (for example, "Pichia Expression Kit" (Invitrogen), pNV11, SP-Q01), and expression vectors derived from *Bacillus subtilis*
15 (for example, pPL608, pKTH50) can be used for producing the protein of the present invention.

[0047]

In order to express the vector in animal cells, such as CHO, COS, or NIH3T3 cells, the vector should have a promoter necessary
20 for expression in such cells, for example, the SV40 promoter (Mulligan et al., Nature (1979) 277, 108), the MMLV-LTR promoter, the EF1 α promoter (Mizushima et al., Nucleic Acids Res. (1990) 18, 5322), the CMV promoter, and the like, and preferably a marker gene for selecting transformants (for example, a drug resistance gene selected
25 by a drug (e.g., neomycin, G418)). Examples of known vectors with these characteristics include, for example, pMAM, pDR2, pBK-RSV, pBK-CMV, pOPRSV, and pOP13.

[0048]

In addition, methods may be used to express a gene stably and,
30 at the same time, to amplify the copy number of the gene in cells. For example, a vector comprising the complementary DHFR gene (for example pCHO I) may be introduced into CHO cells in which the nucleic acid synthesizing pathway is deleted, and then amplified by methotrexate (MTX). Furthermore, in case of transient expression of
35 a gene, the method wherein a vector comprising a replication origin of SV40 (pcD, etc.) is transfected into COS cells comprising the SV40

T antigen expressing gene on the chromosome can be used.

[0049]

The DNA of the present invention can further be expressed *in vivo* in animals, for example, by inserting the DNA of the present invention into an appropriate vector and introducing it into living
5 bodies by methods such as the retrovirus method, the liposome method, the cationic liposome method, and the adenovirus method. In such a manner, gene therapy against diseases attributed to mutation of Gros1 gene of the present invention can be accomplished. As a vector to
10 be used, for example, adenovirus vector (for example pAdexlcw), and retrovirus vector (for example, pZIPneo) can be mentioned, but is not restricted thereto. General gene manipulation, such as insertion of the DNA of the present invention to a vector, can be performed according to conventional methods (Molecular Cloning, 5. 61-5. 63).
15 Administration into a living body can be either an *ex vivo* method, or *in vivo* method.

[0050]

The present invention further relates to a host cell into which the vector of the present invention has been transfected. The host
20 cell into which the vector of the invention is transfected is not particularly limited. For example, *E. coli*, various animal cells and such can be used. The host cells of the present invention can be used, for example, as a production system for producing or expressing the protein of the present invention. The present invention provides
25 methods of producing a protein of the invention both *in vitro* and *in vivo*. For *in vitro* production, eukaryotic cells or prokaryotic cells can be used as host cells.

[0051]

Useful eukaryotic cells may be animal, plant, or fungi cells.
30 Exemplary animal cells include, for example, mammalian cells such as CHO (J. Exp. Med. 108:945 (1995)), COS, 3T3, myeloma, baby hamster kidney (BHK), HeLa, or Vero cells, amphibian cells such as *Xenopus* oocytes (Valle et al. Nature 291:340-358 (1981)), or insect cells such as sf9, sf21, or Tn5 cells. CHO cells lacking DHFR gene
35 (dhfr-CHO) (Proc. Natl. Acad. Sci. U.S.A. 77:4216-4220 (1980)) or CHO K-1 (Proc. Natl. Acad. Sci. U.S.A. 60:1275 (1968)) may also be

used. Of the animal cells, CHO cells are particularly preferable for the mass expression. A vector can be transfected into host cells by, for example, the calcium phosphate method, the DEAE-dextran method, the cationic liposome DOTAP (Boehringer Mannheim), the electroporation method, the lipofection method, and so on.

[0052]

As plant cells, plant cells originating from *Nicotiana tabacum* are known as protein-production systems, and may be used as callus cultures. As fungi cells, yeast cells such as *Saccharomyces*, including *Saccharomyces cerevisiae*, or filamentous fungi such as *Aspergillus*, including *Aspergillus niger*, are known and may be used herein.

[0053]

Useful prokaryotic cells include bacterial cells, such as *E. coli*, for example, JM109, DH5 α , and HB101. Other bacterial systems include, *Bacillus subtilis*.

[0054]

These cells are transformed by a desired DNA, and the resulting transformants are cultured *in vitro* to obtain the protein. Transformants can be cultured using known methods. Culture medium for animal cells include, for example, DMEM, MEM, RPMI1640, or IMDM may be used with or without serum supplement such as fetal calf serum (FCS). The pH of the culture medium is preferably between about 6 and 8. Such cells are typically cultured at about 30 to 40°C for about 15 to 200 hr, and the culture medium may be replaced, aerated, or stirred if necessary.

[0055]

Animal and plant hosts may be used for *in vivo* production. For example, a desired DNA can be transfected into an animal or plant host. Encoded proteins are produced *in vivo*, and then recovered. These animal and plant hosts are included in host cells of the present invention.

[0056]

Animals to be used for the production system described above include, but are not limited to, mammals and insects. Mammals, such as goat, porcine, sheep, mouse, and bovine, may be used (Vicki Glaser,

SPECTRUM Biotechnology Applications (1993)). Alternatively, the mammals may be transgenic animals.

[0057]

For instance, a desired DNA may be prepared as a fusion gene,
5 by fusing it with a gene, such as goat β casein gene which encodes
a protein specifically produced into milk. DNA fragments comprising
the fusion gene are injected into goat embryos, which are then
impregnated into female goats. Proteins are recovered from milk
10 produced by the transgenic goats (i.e., those born from the goats
that had received the modified embryos) or from their offspring. To
increase the amount of milk containing the proteins produced by
transgenic goats, appropriate hormones may be administered to them
(Ebert K. M. et al. Bio/Technology 12:699-702 (1994)).

[0058]

15 Alternatively, insects, such as the silkworm, may be used.
A DNA encoding a desired protein inserted into baculovirus can be
used to transfect silkworms, and the desired protein may be recovered
from their body fluid (Susumu M. et al. Nature 315: 592-594 (1985)).

[0059]

20 As plants, for example, tobacco can be used. In use of tobacco,
a DNA encoding a desired protein may be inserted into a plant
expression vector, such as pMON530, which is introduced into bacteria,
such as *Agrobacterium tumefaciens*. Then, the bacteria is used to
transfect a tobacco plant, such as *Nicotiana tabacum*, and a desired
25 polypeptide is recovered from their leaves (Julian K.-C. Ma et al.,
Eur. J. Immunol. 24: 131-138 (1994)).

[0060]

A protein of the present invention obtained as above may be
isolated from inside or outside (such as medium) of host cells, and
30 purified as a substantially pure homogeneous protein. The method for
protein isolation and purification is not limited to any specific
method; in fact, any standard method may be used. For instance, column
chromatography, filter, ultrafiltration, salt precipitation,
solvent precipitation, solvent extraction, distillation,
35 immunoprecipitation, SDS-polyacrylamide gel electrophoresis,
isoelectric point electrophoresis, dialysis, and recrystallization

may be appropriately selected and combined to isolate and purify the protein.

[0061]

Examples of chromatography include, for example, affinity
5 chromatography, ion-exchange chromatography, hydrophobic
chromatography, gel filtration, reverse phase chromatography,
adsorption chromatography, and such (Strategies for Protein
Purification and Characterization: A Laboratory Course Manual. Ed.
Daniel R. Marshak et al., Cold Spring Harbor Laboratory Press (1996)).
10 These chromatographies may be performed by liquid chromatography,
such as HPLC and FPLC. Thus, the present invention provides for highly
purified proteins prepared by the above methods.

[0062]

A protein of the present invention may be optionally modified
15 or partially deleted by treating it with an appropriate protein
modification enzyme before or after purification. Useful protein
modification enzymes include, but are not limited to, trypsin,
chymotrypsin, lysylendopeptidase, protein kinase, glucosidase and
so on.

20 [0063]

The present invention relates to an antibody that binds to
the protein of the invention. The antibody of the invention can be
used in any form, such as monoclonal or polyclonal antibodies, and
includes antiserum obtained by immunizing an animal such as a rabbit
25 with the protein of the invention, all classes of polyclonal and
monoclonal antibodies, human antibodies, and humanized antibodies
produced by genetic recombination.

[0064]

A protein of the invention used as an antigen to obtain an
30 antibody may be derived from any animal species, but preferably is
derived from a mammal such as a human, mouse, or rat, more preferably
from a human. A human-derived protein may be obtained from the
nucleotide or amino acid sequences disclosed herein.

[0065]

35 According to the present invention, the protein to be used
as an immunization antigen may be a complete protein or a partial

peptide of the protein. A partial peptide may comprise, for example, the amino (N)-terminal or carboxy (C)-terminal fragment of a protein of the present invention. Herein, an antibody is defined as a protein that reacts with either the full length or a fragment of a protein of the present invention.

[0066]

A gene encoding a protein of the invention or its fragment may be inserted into a known expression vector, which is then used to transform a host cell as described herein. The desired protein or its fragment may be recovered from the outside or inside of host cells by any standard method, and may subsequently be used as an antigen. Alternatively, cells expressing the protein or their lysates, or a chemically synthesized protein may be used as the antigen.

[0067]

Any mammalian animal may be immunized with the antigen, but preferably the compatibility with parental cells used for cell fusion is taken into account. In general, animals of Rodentia, Lagomorpha, or Primates are used.

[0068]

Animals of Rodentia include, for example, mouse, rat, and hamster. Animals of Lagomorpha include, for example, rabbit. Animals of Primates include, for example, a monkey of Catarrhini (old world monkey) such as *Macaca fascicularis*, rhesus monkey, sacred baboon, and chimpanzees.

[0069]

Methods for immunizing animals with antigens are known in the art. Intraperitoneal injection or subcutaneous injection of antigens is a standard method for immunization of mammals. More specifically, antigens may be diluted and suspended in an appropriate amount of phosphate buffered saline (PBS), physiological saline, etc. If desired, the antigen suspension may be mixed with an appropriate amount of a standard adjuvant, such as Freund's complete adjuvant, made into emulsion, and then administered to mammalian animals. Preferably, it is followed by several administrations of antigen mixed with an appropriately amount of Freund's incomplete adjuvant every

4 to 21 days. An appropriate carrier may also be used for immunization. After immunization as above, serum is examined by a standard method for an increase in the amount of desired antibodies.

[0070]

5 Polyclonal antibodies against the proteins of the present invention may be prepared by collecting blood from the immunized mammal examined for the increase of desired antibodies in the serum, and by separating serum from the blood by any conventional method. Polyclonal antibodies include serum containing the polyclonal
10 antibodies, as well as the fraction containing the polyclonal antibodies may be isolated from the serum. Immunoglobulin G or M can be prepared from a fraction which recognizes only the protein of the present invention using, for example, an affinity column coupled with the protein of the present invention, and further purifying this
15 fraction by using protein A or protein G column.

[0071]

To prepare monoclonal antibodies, immune cells are collected from the mammal immunized with the antigen and checked for the increased level of desired antibodies in the serum as described above,
20 and are subjected to cell fusion. The immune cells used for cell fusion are preferably obtained from spleen. Other preferred parental cells to be fused with the above immunocyte include, for example, myeloma cells of mammals, and more preferably myeloma cells having an acquired property for the selection of fused cells by drugs.

25 [0072]

The above immunocyte and myeloma cells can be fused according to known methods, for example, the method of Milstein et al. (Galfre, G. and Milstein, C., Methods Enzymol. (1981) 73, 3-46).

[0073]

30 Resulting hybridomas obtained by the cell fusion may be selected by cultivating them in a standard selection medium, such as HAT medium (hypoxanthine, aminopterin, and thymidine containing medium). The cell culture is typically continued in the HAT medium for several days to several weeks, the time being sufficient to allow
35 all the other cells, with the exception of the desired hybridoma (non-fused cells), to die. Then, the standard limiting dilution is

performed to screen and clone a hybridoma cell producing the desired antibody.

[0074]

In addition to the above method in which a non-human animal
5 is immunized with an antigen for preparing hybridoma, a hybridoma
producing a desired human antibody that is able to bind to the protein
can be obtained by the following method. First, human lymphocytes
such as those infected by EB virus may be immunized with a protein,
protein expressing cells, or their lysates *in vitro*. Then, the
10 immunized lymphocytes are fused with human-derived myeloma cells that
are capable of indefinitely dividing, such as U266, to yield the
desired hybridoma (Unexamined Published Japanese Patent Application
No. (JP-A) Sho 63-17688).

[0075]

15 The obtained hybridomas are subsequently transplanted into
the abdominal cavity of a mouse and the ascites are harvested. The
obtained monoclonal antibodies can be purified by, for example,
ammonium sulfate precipitation, a protein A or protein G column, DEAE
ion exchange chromatography, or an affinity column to which the
20 protein of the present invention is coupled. The antibody of the
present invention can be used not only for purification and detection
of the protein of the present invention, but also as a candidate for
agonists and antagonists of the protein of the present invention.
In addition, this antibody can be applied to the antibody treatment
25 for diseases related to the protein of the present invention. When
the obtained antibody is to be administered to the human body (antibody
treatment), a human antibody or a humanized antibody is preferable
for reducing immunogenicity.

[0076]

30 For example, transgenic animals having a repertory of human
antibody genes may be immunized with an antigen selected from a protein,
protein expressing cells, or their lysates. Antibody producing cells
are then collected from the animals and fused with myeloma cells to
obtain hybridoma, from which human antibodies against the protein
35 can be prepared (see WO92-03918, WO93-2227, WO94-02602, WO94-25585,
WO96-33735, and WO96-34096).

[0077]

Alternatively, an immune cell, such as an immunized lymphocyte, producing antibodies may be immortalized by an oncogene and used for preparing monoclonal antibodies.

5 [0078]

Monoclonal antibodies thus obtained can be also recombinantly prepared using genetic engineering techniques (see, for example, Borrebaeck C. A. K. and Larrick J. W. Therapeutic Monoclonal Antibodies, published in the United Kingdom by MacMillan Publishers LTD (1990)). A DNA encoding an antibody may be cloned from an immune cell, such as a hybridoma or an immunized lymphocyte producing the antibody, inserted into an appropriate vector, and introduced into host cells to prepare a recombinant antibody. The present invention also provides recombinant antibodies prepared as described above.

15 [0079]

Furthermore, an antibody of the present invention may be a fragment of an antibody or modified antibody, so long as it binds to one or more of the proteins of the invention. For instance, the antibody fragment may be Fab, F(ab')₂, Fv, or single chain Fv (scFv), in which Fv fragments from H and L chains are ligated by an appropriate linker (Huston J. S. et al. Proc. Natl. Acad. Sci. U.S.A. 85:5879-5883 (1988)). More specifically, an antibody fragment may be generated by treating an antibody with an enzyme, such as papain or pepsin. Alternatively, a gene encoding the antibody fragment may be constructed, inserted into an expression vector, and expressed in an appropriate host cell (see, for example, Co M. S. et al. J. Immunol. 152:2968-2976 (1994); Better M. and Horwitz A. H. Methods Enzymol. 178:476-496 (1989); Pluckthun A. and Skerra A. Methods Enzymol. 178:497-515 (1989); Lamoyi E. Methods Enzymol. 121:652-663 (1986); Rousseaux J. et al. Methods Enzymol. 121:663-669 (1986); Bird R. E. and Walker B. W. Trends Biotechnol. 9:132-137 (1991)).

30 [0080]

An antibody may be modified by conjugation with a variety of molecules, such as polyethylene glycol (PEG). The present invention provides for such modified antibodies. The modified antibody can be obtained by chemically modifying an antibody. These modification

methods are conventional in the field.

[0081]

Alternatively, an antibody of the present invention may be obtained as a chimeric antibody, between a variable region derived from nonhuman antibody and the constant region derived from human antibody, or as a humanized antibody, comprising the complementarity determining region (CDR) derived from nonhuman antibody, the framework region (FR) derived from human antibody, and the constant region. Such antibodies can be prepared by using known technology.

[0082]

Antibodies obtained as above may be purified to homogeneity. For example, the separation and purification of the antibody can be performed according to separation and purification methods used for general proteins. For example, the antibody may be separated and isolated by the appropriately selected and combined use of column chromatographies, such as affinity chromatography, filter, ultrafiltration, salting-out, dialysis, SDS polyacrylamide gel electrophoresis, isoelectric focusing, and others (Antibodies: A Laboratory Manual. Ed Harlow and David Lane, Cold Spring Harbor Laboratory, 1988), but are not limited thereto.

[0083]

A protein A column and protein G column can be used as the affinity column. Exemplary protein A columns to be used include, for example, Hyper D, POROS, and Sepharose F.F. (Pharmacia).

[0084]

Exemplary chromatography, with the exception of affinity includes, for example, ion-exchange chromatography, hydrophobic chromatography, gel filtration, reverse-phase chromatography, adsorption chromatography, and the like (Strategies for Protein Purification and Characterization: A Laboratory Course Manual. Ed Daniel R. Marshak et al., Cold Spring Harbor Laboratory Press, 1996). The chromatographic procedures can be carried out by liquid-phase chromatography, such as HPLC, FPLC.

[0085]

For example, measurement of absorbance, enzyme-linked immunosorbent assay (ELISA), enzyme immunoassay (EIA),

radioimmunoassay (RIA), and/or immunofluorescence may be used to measure the antigen binding activity of the antibody of the invention. In ELISA, the antibody of the present invention is immobilized on a plate, protein of the invention is applied to the plate, and then
5 a sample containing a desired antibody, such as culture supernatant of antibody producing cells or purified antibodies, is applied. Then, a secondary antibody that recognizes the primary antibody and is labeled with an enzyme, such as alkaline phosphatase, is applied, and the plate is incubated. Next, after washing, an enzyme substrate,
10 such as *p*-nitrophenyl phosphate, is added to the plate, and the absorbance is measured to evaluate the antigen binding activity of the sample. A fragment of the protein, such as a C-terminal or N-terminal fragment may be used as a protein. BIAcore (Pharmacia) may be used to evaluate the activity of the antibody according to
15 the present invention.

[0086]

The above methods allow for the detection or measurement of the protein of the invention, by exposing the antibody of the invention to a sample assumed to contain the protein of the invention, and
20 detecting or measuring the immune complex formed by the antibody and the protein.

[0087]

Because the method of detection or measurement of the protein according to the invention can specifically detect or measure a
25 protein, the method may be useful in a variety of experiments in which the protein is used.

[0088]

The present invention also relates to a DNA which hybridizes with the DNA encoding human or mouse Gros1 protein (SEQ ID NOs: 1,
30 3, 5, or 7) or a DNA complementary to the DNA, and which comprises at least 15 nucleotides. The term "specifically hybridize" as used herein, means that cross-hybridization does not occur significantly with DNA encoding other proteins, under the usual hybridizing conditions, preferably under stringent hybridizing conditions. Such
35 DNAs include, probes, primers, nucleotides and nucleotide derivatives (for example, antisense oligonucleotides and ribozymes), which

specifically hybridize with DNA encoding the protein of the invention or DNA complementary to the DNA. Moreover, such DNA can be utilized for the preparation of DNA chip.

[0089]

5 The present invention includes an antisense oligonucleotide that hybridizes with any site within the nucleotide sequence any one of SEQ ID NO: 1, 3, 5 or 7. This antisense oligonucleotide is preferably against at least 15 continuous nucleotides of the nucleotide sequence any one of SEQ ID NO: 1, 3, 5 or 7. The
10 above-mentioned antisense oligonucleotide, which contains an initiation codon in the above-mentioned at least 15 continuous nucleotides, is even more preferred.

[0090]

Derivatives or modified products of antisense
15 oligonucleotides can be used as antisense oligonucleotides. Examples of such modified products include lower alkyl phosphonate modifications such as methyl-phosphonate-type or ethyl-phosphonate-type, phosphorothioate modifications and phosphoroamidate modifications.

20 [0091]

The term "antisense oligonucleotides" as used herein means, not only those in which the nucleotides corresponding to those constituting a specified region of a DNA or mRNA are entirely complementary, but also those having a mismatch of one or more
25 nucleotides, as long as the DNA or mRNA and the antisense oligonucleotide can specifically hybridize with the nucleotide sequence of SEQ ID NO: 1, 3, 5 or 7.

[0092]

Such DNAs are contained as those having, in the "at least 15
30 continuous nucleotide sequence region", a homology of at least 70% or higher, preferably at 80% or higher, more preferably 90% or higher, even more preferably 95% or higher. The algorithm stated herein can be used to determine the homology. Such DNAs are useful as probes for the isolation or detection of DNA encoding the protein of the
35 invention as stated in a later example or as a primer used for amplifications.

[0093]

The antisense oligonucleotide derivatives of the present invention act upon cells producing the protein of the invention by binding to the DNA or mRNA encoding the protein, inhibiting its transcription or translation, promoting the degradation of the mRNA, and inhibiting the expression of the protein of the invention, thereby resulting in the inhibition of the protein's function.

[0094]

An antisense oligonucleotide derivative of the present invention can be made into an external preparation, such as a liniment or a poultice, by mixing with a suitable base material which is inactive against the derivatives.

[0095]

Also, as needed, the derivatives can be formulated into tablets, powders, granules, capsules, liposome capsules, injections, solutions, nose-drops and freeze-drying agents by adding excipients, isotonic agents, solubilizers, stabilizers, preservatives, pain-killers, and such. These can be prepared by following usual methods.

[0096]

The antisense oligonucleotide derivative is given to the patient by directly applying onto the ailing site or by injecting into a blood vessel so that it will reach the site of ailment. An antisense-mounting medium can also be used to increase durability and membrane-permeability. Examples are, liposome, poly-L-lysine, lipid, cholesterol, lipofectin or derivatives of these.

[0097]

The dosage of the antisense oligonucleotide derivative of the present invention can be adjusted suitably according to the patient's condition and used in desired amounts. For example, a dose range of 0.1 to 100 mg/kg, preferably 0.1 to 50 mg/kg can be administered.

[0098]

The antisense oligonucleotide of the invention inhibits the expression of the protein of the invention and is thereby useful for suppressing the biological activity of the protein of the invention. Also, expression-inhibitors, comprising the antisense

oligonucleotide of the invention, are useful in the point that they can inhibit the biological activity of the protein of the invention.

[0099]

Moreover, the present invention relates to a method of
5 screening for a compound that binds to the protein of the present invention by using the protein of the present invention. This screening method comprises the steps of: (a) contacting the protein of the present invention or a partial peptide thereof with a subject sample, (b) detecting the binding activity between the protein of
10 the present invention or the partial peptide thereof and the subject sample, and (c) selecting a compound that binds to the protein of the present invention or the partial peptide thereof.

[0100]

The protein of the present invention to be used for screening
15 may be a recombinant protein or a protein derived from the nature, or a partial peptide thereof. Any subject sample, for example, cell extracts, cell culture supernatant, products of fermenting microorganism, extracts from marine organism, plant extracts, purified or crude proteins, peptides, non-peptide compounds,
20 synthetic micromolecular compounds and natural compounds, can be used. The protein of the present invention to be contacted with a subject sample can be, for example, a purified protein, a soluble protein, a form bound to a carrier, or a fusion protein fused with other proteins.

25 [0101]

As a method of screening for proteins, for example, that bind to the protein of the present invention using the protein of the present invention, many methods well known by a person skilled in the art can be used. Such a screening can be conducted by, for example,
30 immunoprecipitation method, specifically, in the following manner. The gene encoding the protein of the present invention is expressed in animal cells and so on by inserting the gene to an expression vector for foreign genes, such as pSV2neo, pcDNA I, and pCD8. The promoter to be used for the expression may be any promoter that can be used
35 commonly and include, for example, the SV40 early promoter (Rigby in Williamson (ed.), Genetic Engineering, vol. 3. Academic Press,

London, p. 83-141 (1982)), the EF-1 α promoter (Kim et al., Gene 91, p217-223 (1990)), the CAG promoter (Niwa et al. Gene 108, p. 193-200 (1991)), the RSV LTR promoter (Cullen Methods in Enzymology 152, p. 684-704 (1987)) the SR α promoter (Takebe et al., Mol. Cell. Biol. 8, p. 466 (1988), the CMV immediate early promoter (Seed and Aruffo Proc. Natl. Acad. Sci. USA 84, p. 3365-3369 (1987)), the SV40 late promoter (Gheysen and Fiers J. Mol. Appl. Genet. 1, p. 385-394 (1982)), the Adenovirus late promoter (Kaufman et al., Mol. Cell. Biol. 9, p. 946 (1989)), the HSV TK promoter and so on. The introduction of the gene into animal cells to express a foreign gene can be performed according to any methods, for example, the electroporation method (Chu G. et al. Nucl. Acids Res. 15, 1311-1326 (1987)), the calcium phosphate method (Chen, C and Okayama, H. Mol. Cell. Biol. 7, 2745-2752 (1987)), the DEAE dextran method (Lopata, M. A. et al. Nucl. Acids Res. 12, 5707-5717 (1984)), Sussman, D. J. and Milman, G. Mol. Cell. Biol. 4, 1642-1643 (1985)), the Lipofectin method (Derijard, B. Cell 7, 1025-1037 (1994); Lamb, B. T. et al. Nature Genetics 5, 22-30 (1993); Rabindran, S. K. et al. Science 259, 230-234 (1993)), and so on. The protein of the present invention can be expressed as a fusion protein comprising a recognition site (epitope) of a monoclonal antibody by introducing the epitope of the monoclonal antibody, whose specificity has been revealed, to the N- or C- terminus of the protein of the present invention. A commercially available epitope-antibody system can be used (Experimental Medicine 13, 85-90 (1995)). Vectors which can express a fusion protein with, for example, β -galactosidase, maltose binding protein, glutathione S-transferase, green florescence protein (GFP) and so on by the use of its multiple cloning sites are commercially available.

[0102]

A fusion protein prepared by introducing only small epitopes consisting of several to a dozen amino acids so as not to change the property of the protein of the present invention by the fusion is also reported. Epitopes, such as polyhistidine (His-tag), influenza aggregate HA, human c-myc, FLAG, Vesicular stomatitis virus glycoprotein (VSV-GP), T7 gene 10 protein (T7-tag), human simple herpes virus glycoprotein (HSV-tag), E-tag (an epitope on monoclonal

phage), and such, and monoclonal antibodies recognizing them can be used as the epitope-antibody system for screening proteins binding to the protein of the present invention (Experimental Medicine 13, 85-90 (1995)).

5 [0103]

In immunoprecipitation, an immune complex is formed by adding these antibodies to cell lysate prepared by using an appropriate detergent. The immune complex consists of the protein of the present invention, a protein comprising the binding ability with the protein, and an antibody. Immunoprecipitation can be also conducted by using antibodies against the protein of the present invention, besides using antibodies against the above epitopes. An antibody against the protein of the present invention can be prepared, for example, by introducing a gene encoding the protein of the present invention to an appropriate *E. coli* expression vector, expressing the gene in *E. coli*, purifying the expressed protein, and immunizing rabbits, mice, rats, goats, domestic fowls and such against the protein. The antibody can be also prepared by immunizing the above animals against a synthesized partial peptide of the protein of the present invention.

20 [0104]

An immune complex can be precipitated, for example by Protein A Sepharose or Protein G sepharose when the antibody is a mouse IgG antibody. If the protein of the present invention is prepared as a fusion protein with an epitope, such as GST, an immune complex can be formed in the same manner as in the use of the antibody against the protein of the present invention, by using a substance specifically binding to these epitopes, such as glutathione-Sepharose 4B.

[0105]

30 Immunoprecipitation can be performed by following or according to, for example, the methods in the literature (Harlow, E. and Lane, D.: Antibodies pp. 511-552, Cold Spring Harbor Laboratory publications, New York (1988))

[0106]

35 SDS-PAGE is commonly used for analysis of immunoprecipitated proteins and the bound protein can be analyzed by the molecular weight

of the protein by using gels with an appropriate concentration. Since the protein bound to the protein of the present invention is difficult to detect by a common staining method, such as Coomassie staining or silver staining, the detection sensitivity for the protein can be improved by culturing cells in culture medium containing radioactive isotope, ^{35}S -methionine or ^{35}S -cystein, labeling proteins in the cells, and detecting the proteins. The target protein can be purified directly from the SDS-polyacrylamide gel and its sequence can be determined, when the molecular weight of a protein has been revealed.

[0107]

As a method for isolating proteins binding to the protein of the present invention by using the protein, for example, West-Western blotting analysis (Skolnik, E. Y. et al., Cell (1991) 65, 83-90) can be used. Specifically, a protein binding to the protein of the present invention can be obtained by preparing a cDNA library from cells, tissues, organs (for example, tissues such as ovary, testis, and placenta or cultured cells) expected to express a protein binding to the protein of the present invention by using a phage vector ($\lambda\text{gt}11$, ZAP, etc.), expressing the protein on LB-agarose, fixing the protein expressed on a filter, reacting the purified and labeled protein of the present invention with the above filter, and detecting the plaques expressing proteins bound to the protein of the present invention according to the label. The protein of the invention may be labeled by utilizing the binding between biotin and avidin, or by utilizing an antibody that specifically binds to the protein of the present invention, or a peptide or polypeptide (for example, GST) that is fused to the protein of the present invention. Methods using radioisotope or fluorescence and such may be also used.

[0108]

Alternatively, in another embodiment of the screening method of the present invention, a two-hybrid system utilizing cells may be used ("Fields S. and Sternglanz R. Trends Genet. (1994) 10:286-292").

[0109]

The protein of the invention is fused to the SRF-binding region

or GAL4-binding region and expressed in yeast cells. A cDNA library is prepared from cells expected to express a protein binding to the protein of the invention, such that the library, when expressed, is fused to the VP16 or GAL4 transcriptional activation region. The cDNA library is then introduced into the above yeast cells, and the cDNA derived from the library is isolated from the positive clones detected. The cDNA is then introduced and expressed in *E. coli*. (when a protein binding to the protein of the invention is expressed in yeast cells, the binding of the two activates a reporter gene, making positive clones detectable.) By using "two-hybrid system" ("MATCHMAKER Two-Hybrid system", "Mammalian MATCHMAKER Two-Hybrid Assay Kit", "MATCHMAKER One-Hybrid system" (Clontech); "HybriZAP Two-Hybrid Vector System" (Stratagene); the reference "Dalton S, and Treisman R (1992) "Characterization of SAP-1, a protein recruited by serum response factor to the c-fos serum response element." Cell 68, 597-612"), a protein which binds to the protein of the present invention or a gene thereof can be prepared.

[0110]

As a reporter gene, for example, Ade2 gene, lacZ gene, CAT gene, luciferase gene and such can be used besides HIS3 gene.

[0111]

A compound binding to the protein of the present invention can be screened using affinity chromatography. For example, the protein of the invention may be immobilized on a carrier of an affinity column, and a test sample, containing a protein capable of binding to the protein of the invention is supposed to be expressed, is applied to the column. A test sample herein may be, for example, cell extracts, cell lysates, etc. After loading the test sample, the column is washed, and proteins bound to the protein of the invention can be prepared.

[0112]

The amino acid sequence of the obtained protein is analyzed, an oligo DNA is synthesized based on the sequence, and cDNA libraries are screened using the oligo DNA as a probe to obtain a DNA encoding the protein.

[0113]

A biosensor using the surface plasmon resonance phenomenon

may be used as a mean for detecting or quantifying the bound compound in the present invention. When such a biosensor is used, the interaction between the protein of the invention and a test compound can be observed real-time as a surface plasmon resonance signal, using
5 only a minute amount of protein and without labeling (for example, BIAcore, Pharmacia). Therefore, it is possible to evaluate the binding between the protein of the invention and a test compound using a biosensor such as BIAcore.

[0114]

10 The methods of screening for molecules that bind when the immobilized protein of the present invention is exposed to synthetic chemical compounds, or natural substance banks, or a random phage peptide display library, or the methods of screening using high-throughput based on combinatorial chemistry techniques
15 (Wrighton Nc, Farrel FX, Chang R, Kashyap AK, Barbone FP, Mulcahy LS, Johnson DL, Barret RW, Jolliffe LK, Dower WJ; Small peptides as potent mimetics of the protein hormone erythropoietin, Science (UNITED STATES) Jul 26 1996, 273 p458-64, Verdine GL., The combinatorial chemistry of nature. Nature (ENGLAND) Nov 7 1996, 384, p11-13, Hogan JC Jr., Directed combinatorial chemistry. Nature (ENGLAND) Nov 7 1996, 384 p17-9) to isolate not only proteins but
20 chemical compounds that bind to protein of the present invention (including agonist and antagonist) are well known to one skilled in the art.

25 [0115]

A compound isolated by the screening is a candidate for drugs which promote or inhibit the activity of the protein of the present invention, for treating or preventing diseases attributed to, for example, the functional abnormality of the protein of the present
30 invention, or cell proliferative diseases such as cancer. A compound in which a part of the structure of the compound obtained by the present screening method having the activity of binding to the protein of the present invention is converted by addition, deletion and/or replacement, is included in the compounds obtained by the screening
35 method of the present invention.

[0116]

Moreover the present invention relates to a method for screening a compound which promotes or inhibits the activity of the protein of the present invention. Since the Gros1 protein of the present invention has the activity of inhibiting cell proliferation, a compound which promotes or inhibits this activity of Gros1 protein of the present invention can be screened using this activity as an index.

[0117]

This screening method includes the steps of: (a) culturing cells which express Gros1 protein in the presence of the subject sample, (b) detecting the proliferation of the cells, and (c) selecting a compound which promotes or inhibits the proliferation in comparison with the proliferation detected in the absence of the subject sample.

[0118]

Any Gros1 proteins can be used for screening so long as they comprise the activity of inhibiting cell proliferation. For example, human or mouse Gros1-L protein can be used and proteins functionally equivalent to these proteins can also be used. Gros1 proteins may be expressed endogenously or exogenously by cells.

[0119]

Any subject samples, for example, cell extracts, cell culture supernatant, products of fermenting microorganism, extracts of marine organism, plant extracts, purified or crude proteins, peptides, non-peptide compounds, synthetic micromolecular compounds, natural compounds, can be used. A compound obtained by the above screening for compounds that bind to the protein of the present invention can be also used as the subject compound.

[0120]

The compound isolated by this screening is a candidate for agonists or antagonists of the protein of the present invention. The term "agonist" refers to molecules that activate the function of the protein of the present invention by binding thereto. Likewise, the term "antagonist" refers to molecules that inhibit the function of the protein of the present invention by binding thereto. Moreover, a compound isolated by this screening is a candidate for compounds which inhibit the *in vivo* interaction of the protein of the present

invention with molecules (including DNAs and proteins) .

[0121]

Cell proliferation can be detected, for example, by determining the speed of cell proliferation, measuring the cell cycle and such, as well as by measuring the colony forming activity as described in the Examples.

[0122]

The compound isolated by the screening is a candidate for drugs which promote or inhibit the activity of the protein of the present invention and can be applied to the treatment for diseases (for example, cancer, etc.) associated with the protein of the present invention.

[0123]

Moreover, compound in which a part of the structure of the compound promoting or inhibiting the activity of Gros1 proteins is converted by addition, deletion and/or replacement are also included in the compounds obtainable by the screening method of the present invention.

[0124]

When administrating the compound isolated by the method of the invention as a pharmaceutical for humans and other mammals, such as mice, rats, guinea-pigs, rabbits, chicken, cats, dogs, sheep, pigs, cattle, monkeys, baboons, chimpanzees, the isolated compound can be directly administered or can be formulated into a dosage form using known pharmaceutical preparation methods. For example, according to the need, the drugs can be taken orally, as sugar-coated tablets, capsules, elixirs and microcapsules, or non-orally, in the form of injections of sterile solutions or suspensions with water or any other pharmaceutically acceptable liquid. For example, the compounds can be mixed with pharmacologically acceptable carriers or medium, specifically, sterilized water, physiological saline, plant-oil, emulsifiers, suspending agents, surfactants, stabilizers, flavoring agents, excipients, vehicles, preservatives, binders and such, in a unit dose form required for generally accepted drug implementation. The amount of active ingredients in these preparations makes a suitable dosage within the indicated range acquirable.

[0125]

Examples of additives that can be mixed to tablets and capsules are, binders such as gelatin, corn starch, tragacanth gum and arabic gum; excipients such as crystalline cellulose; swelling agents such as corn starch, gelatin and alginic acid; lubricants such as magnesium stearate; sweeteners such as sucrose, lactose or saccharin; flavoring agents such as peppermint, Gaultheria adeno-thrix oil and cherry. When the unit dosage form is a capsule, a liquid carrier, such as oil, can also be further included in the above ingredients. Sterile composites for injections can be formulated following normal drug implementations using vehicles such as distilled water used for injections.

[0126]

Physiological saline, glucose, and other isotonic liquids including adjuvants, such as D-sorbitol, D-mannnose, D-mannitol, and sodium chloride, can be used as aqueous solutions for injections. These can be used in conjunction with suitable solubilizers, such as alcohol, specifically ethanol, polyalcohols such as propylene glycol and polyethylene glycol, non-ionic surfactants, such as Polysorbate 80 (TM) and HCO-50.

[0127]

Sesame oil or Soy-bean oil can be used as a oleaginous liquid and may be used in conjunction with benzyl benzoate or benzyl alcohol as a solubilizers and may be formulated with a buffer, such as phosphate buffer and sodium acetate buffer; a pain-killer, such as procaine hydrochloride; a stabilizer, such as benzyl alcohol, phenol; and an anti-oxidant. The prepared injection may be filled into a suitable ampule.

[0128]

Methods well known to one skilled in the art may be used to administer the inventive pharmaceutical compound to patients, for example as intraarterial, intravenous, percutaneous injections and also as intranasal, transbronchial, intramuscular or oral administrations. The dosage and method of administration vary according to the body-weight and age of a patient and the administration method; however, one skilled in the art can routinely select them. If said compound is encodable by a DNA, the DNA can be

inserted into a vector for gene therapy and the vector administered to perform the therapy. The dosage and method of administration vary according to the body-weight, age, and symptoms of a patient but one skilled in the art can select them suitably.

5 [0129]

For example, although there are some differences according to the symptoms, the dose of a compound that binds with the protein of the present invention and regulates its activity is about 0.1 mg to about 100 mg per day, preferably about 1.0 mg to about 50 mg per day
10 and more preferably about 1.0 mg to about 20 mg per day, when administered orally to a normal adult (weight 60 kg).

[0130]

When administering parenterally, in the form of an injection to a normal adult (weight 60 kg), although there are some differences
15 according to the patient, target organ, symptoms and method of administration, it is convenient to intravenously inject a dose of about 0.01 mg to about 30 mg per day, preferably about 0.1 to about 20 mg per day and more preferably about 0.1 to about 10 mg per day. Also, in the case of other animals too, it is possible to administer
20 an amount converted to 60kgs of body-weight.

[0131]

The present invention is illustrated in details by following Examples, but is not restricted to these Examples.

[0132]

25 [Examples]

Example 1: Cloning and sequence of Gros1 cDNA

It is known that the comparison of the proteins contained in the Triton X-100 insoluble factions of the plasma membrane of mouse normal cells (CMEF) and immortalized cells (NIH3T3) revealed that
30 the protein (p33), about 30 kDa in size, present in NIH3T3 is not contained in CMEF (Wadhwa, R. et al (1991) Mutat. Res. 256, 243-54). This protein was isolated by SDS-PAGE and anti-p33 polyclonal antibody was prepared by a standard method. A novel gene Gros1-L was obtained from an RS-4 cell cDNA library (Wadhwa, R. et al (1993) J. Biol. Chem.
35 268, 6615-21) by immunoscreening using this antibody. The sequence of this gene was novel, and no homologous sequences were found in

the DNA sequence data bank. Screening of the human testis library (prepared based on pCMV-SPORT (GIBCO BRL Cat#. 10419-018); D'Alessio et al., 1990, Focus 12, 47; Kriegler, M., 1990, Gene Transfer and Expression: A Laboratory Manual, Stockton Press, New York, NY.;
5 Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd Edition. Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.; Li, W.-B. et al., 1994, BioTechniques 16, 722) using a ³²P labeled mouse Gros1 probe identified two types of clones (human Gros1-L and Gros1-S). Mouse Gros1-S was identified by searching the EST data
10 using the nucleotide sequences of the obtained mouse Gros1 cDNA fragments and connecting overlapped clones (Figure 1). This EST contained a 94 bp deletion in comparison with mouse Gros1-L or other ESTs, and was predicted to generate a protein (mouse Gros1-S) shorter than the non-deleted type (mouse Gros1-L).

15 [0133]

SEQ ID NOs: 5 and 7 show the full length nucleotide sequences of mouse Gros1-L cDNA and the full length nucleotide sequence of mouse Gros1-S cDNA obtained by the cloning using EST search, respectively. Amino acid sequences deduced from these nucleotide sequences are shown
20 in SEQ ID NOs: 6 and 8, respectively. No homology was found in the DNA sequence data bank. The cDNA obtained by immunoscreening (mouse Gros1-L) and the cDNA obtained by the cloning using EST search encoded a mouse Gros1-S, an 85 kDa protein consisting of 747 amino acids and a 61.5 kDa protein consisting of 542 amino acids (Figure 2),
25 respectively, no corresponding within the protein database significantly. Moreover, the above human 3.0 Kb clone cDNA (SEQ ID NO: 1) and the cDNA of 2.7 kb clone (SEQ ID NO: 3) having 83.9 % homology with the mouse Gros1 were not found homology in the DNA sequence data bank. The obtained 3.0 Kb clone cDNA (SEQ ID NO: 1) encoded human
30 Gros1-S of 41 kDa consisting of 363 amino acids (SEQ ID NO: 2), and the 2.7 Kb clone cDNA (SEQ ID NO: 3) encoded human Gros1-L of 83 kDa consisting of 736 amino acids (SEQ ID NO: 4) (Figure 3), each no corresponding within the protein database. Although no matching DNA sequences were found, analysis of amino acid sequences by motif search
35 revealed that the amino acid sequences in mouse and human Gros1-L partially comprise the leucine zipper structure frequently found in

transcriptional factors.

[0134]

Example 2: Preparation of recombinant Gros1

The cDNA at 183-1055 within the mouse Gros1-L cDNA open reading
5 frame was amplified by the PCR reaction (94°C for 1 min, 55°C for 1
min, and 72°C for 3 min, 25 cycles) using a sense primer comprising
the BamHI site (SEQ ID NO: 9) and an antisense primer comprising the
HindIII site (SEQ ID NO: 10), and the obtained product was inserted
10 into pGEM-T easy vector (Promega) using Rapid Ligation Kit (Boehringer
Mannheim). The mixture solution of *E. coli* JM109 competent cells
(TOYOBO) and the vector were treated at 42°C for 1 min, spread on an
ampicillin plate, and cultured for 1 day, and colonies were collected
for cloning. To prepare the histidine-tagged protein, the cloned
pGEM-T/Gros1 vector was cleaved at BamH I-Hind III sites, ligated
15 with pQE30 (Qiagen), and digested at the same restriction sites by
the same manner as above, and colonies were collected to obtain
plasmids. *E. coli* M15 (Qiagen) was cultured until the absorbance at
580 nm reached 0.6, at which point the cells were transformed by the
collected plasmids, and proteins were produced by inducing at 37°C
20 for 3 hours with 0.2 mM IPTG. Lysate of this *E. coli* was separated
by SDS-PAGE method and detection was conducted by the Western blot
analysis with the histidine antibody and Gros1 antibody described
below. As a result, it was confirmed that a 40 kDa protein was
synthesized. The size of the recombinant protein was as predicted.
25 No signals could be detected by the Western blot analysis using the
anti-p33 polyclonal antibody in the same manner.

[0135]

Example 3: Northern blot analysis

Northern blot analysis was conducted by purchasing a membrane
30 on which 2 µg of mRNA from various mouse, human tissues per lane were
loaded (Clontech laboratories, Palo alto, CA). The gene fragment of
mouse Gros1-L plasmid was used as a probe. Condition for the
hybridization was as follows: "Rapid-hyb buffer" (Amersham LIFE
SCIENCE) was used, and after prehybridization at 68°C for 30 min, the
35 labeled probes were added, and the solution was incubated at 68°C
for 2 hours to perform hybridization. Then washing was conducted 3

times in 2X SSC, 0.01% SDS at room temperature for 20 min, then 3 times in 1X SSC, 0.1% SDS at 37°C for 20 min, and twice in 1X SSC, 0.1% SDS at 50°C for 20 min. Detection was performed by autoradiography. Northern blot analysis showed that the 4.4 kb and 2.5 kb bands were weakly expressed in most tissues in human, except for testis, ovary, and placenta. In contrast, in testis, ovary, and placenta, very strong expression was observed (Figure 4). Higher expression of mRNA in human cultured cells was observed than in tissues. Moreover, in human normal cultured cells, the expression amount of the 2.5 kb mRNA was nearly 10 times as high as that for the mRNA of 4.4 kb (Figure 5). In mouse, the 3.5 kb and 2.5 kb bands were weakly expressed in most tissues, except for brain, spleen and testis. No expression was observed in brain or spleen, and in testis only the 2.5 kb band was expressed. In testis and ovary, only the short type of Gros1 mRNAs was detected. It was shown that the expression dramatically disappeared at the 11th day during developmental process (Figure 6).

[0136]

Example 4: Location on the chromosomes

The locations of the genes of the present invention were determined by using a sense primer (SEQ ID NO: 11) and an antisense primer (SEQ ID NO: 12) specific to human Gros1, with a radiation hybrid panel. As a result, they were found to be present on chromosome 1p31 in human. In mouse, they were deduced to be present on chromosome 4.

[0137]

Example 5: Preparation of antibodies specifically binding to the Gros1 proteins

Antibodies against the recombinant protein deduced from the gene sequence of Gros1 were prepared. Specifically, the recombinant mouse Gros1-L protein with the histidine-tag prepared in Example 2 was purified by a nickel column; rabbits were immunized to extract the serum 4 times stepwise; and, finally, exsanguinations were conducted. Polyclonal antibodies were prepared by purifying this serum using the protein A column. It was confirmed that this anti-Gros1 polyclonal antibody recognizes Gros1 protein by separating

the recombinant histidine-tagged human Gros1-L protein on the gel by SDS-PAGE, and detecting by the Western blot analysis.

[0138]

Example 6: Western blot analysis

5 Western blot analysis on the lysate of human normal lung fibroblast cell, MRC-5, with the above Gros1 polyclonal antibodies detected a band about 83 kDa and another about 41 kDa which were expected from the cDNA sequence. The fact that two bands were detected is consistent with the fact that two types of transcripts, one of 10 about 4.4 and the other of about 2.5 kb, respectively, were detected in the Northern analysis. Interestingly, in HeLa cells, in which only the long band was detected by Northern analysis, only the 83 kDa band was detected by the Western analysis. On the other hand, in NIH3T3 cells, not only the band of about 85 kDa was detected by anti-Gros1 15 antibody, but also bands with the size of 61.5, 41, 34 and 32 kDa were detected. The bands of about 85 kDa and 61.5 kDa correspond to mouse Gros1-L and mouse Gros1-S, respectively, and the other bands correspond presumably to proteins cleaved or modified endogenously. In COS7 cells, 60, 40 and 34 kDa bands were detected. The cDNAs 20 encoding either human Gros1-L or S were inserted into expression vectors and transfected into COS7 cells. As the expression vector, pCMV-SPORT Vector (GIBCO BRL) used in the screening of human testis library was used. As a result of Western blot analysis using anti-Gros1 antibody, either an 83 kDa band or 41 kDa band corresponding 25 to the cDNA sequence was detected. In COS7 cells, in which this plasmid encoding GFP-Gros1 fusion protein described below was transfected, production of proteins corresponding to the sizes of Gros1-L or Gros1-S (115 kDa and 72 kDa, respectively) was confirmed by Western blot analysis after SDS-PAGE.

30 [0139]

Example 7: Localization of the genes in the cell

Two types of human Gros1 cDNA were amplified by PCR using sense (SEQ ID NO: 13) and antisense (SEQ ID NO: 14, 15) primers designed so as to comprise two types of open reading frames corresponding to 35 human Gros1-L and S. "GFPC1/7-3.0", which expresses the fusion protein of human Gros1-S, and "GFPC1/7-2.7", which expresses the

fusion protein of human Gros1-L, were prepared by inserting these genes to the C terminal region of GFP ORF in pEGFP-C1 (Clontech). With the usage of Tfx-50 (Promega), these plasmids encoding the GFP-Gros1 fusion protein and the controls plasmids encoding only the GFP were transfected into COS7 cells growing on the cover glass. The cells were fixed with 4% formaldehyde, 24 hours after the transfection, and were washed three times with PBS. The cells were observed with an epifluorescence Olympus BH-2 microscope. As a result, the two types of proteins fused with different types of Gros1 full-length sequences were both localized in the cytoplasm (Figures 7 and 8).

[0140]

Example 8: Proliferation repressing activity

The Gros1 mutant cDNA/pBluescript encoding only the 369 amino acids at the N-terminus of mouse Gros1-L isolated by screening was cleaved with EcoRI, and ligated in the same manner as in Example 2, with SR α expression vector (Mol. Cell. Biol. (1988) 8, 466-472), and treated with the restriction enzyme EcoRI. As a result, two clones, in sense and antisense directions, respectively, were obtained. To isolate a gene encoding the full-length mouse Gros1, EST clone AA49892A, which showed homology with mouse Gros1, was purchased from Genome System. The EST clone and Gros1 cDNA/pBluescript were both treated with restriction enzymes ScaI and NotI, and the gene fragments were ligated in the same manner as in Example 2 to obtain the mouse Gros1-L gene. This Gros1-L gene fragment was further treated with restriction enzymes at the EcoRI-NotI site and ligated to the SR α expression vector treated with restriction enzymes at the same site in the same manner as in Example 2. As a result, the SR α /Gros 1-L sense clone which expresses mouse Gros1-L was isolated.

[0141]

Six G418 resistance clones were obtained by introducing the above vectors into NIH3T3 cells and expression of Gros1 in each vector was confirmed by Northern blot analysis (Figure 9). Among these, a clone in sense direction with especially high expression and a clone in antisense direction in which endogenous Gros1 transcript was rarely detected by Northern analysis were subjected to the colony forming activity test.

[0142]

500 cells of each clone were spread on a 10 cm dish, and cultured for 2 weeks by replacing the medium once every three days. The cells were fixed with PBS containing 4% formaldehyde and stained with methylene blue to count the number of colonies. The experiments were done in triplicate.

[0143]

As a result, whereas colony formation was extremely delayed in clones transfected with Gros1-L in the sense direction, the colony formation in clones transfected with Gros1-L in the antisense direction was as about 5 times higher than the control (Figure 10, Table 1). In Gros1-mutant in the sense direction, no decrease of colony formation was observed ("defective colonies" in Table 1). From results above, Gros1 protein was shown to have an activity to repress proliferation.

[0144]

[Table 1]

Cloned Cell	Number of colonies	
	Dish 1	Dish 2
Control colonies		
Control 702	197	150
Control 733	223	106
Sense colonies		
NIH3T3/7-7m3 S2	38	42
NIH3T3/7-7m3 S4	23	40
NIH3T3/7-7m3 S5	40	60
NIH3T3/7-7m3 S6	33	9
NIH3T3/7-7m3 S10	39	16
Antisense colonies		
#723	181	186
#AS1	190	169
#AS2	276	336
#AS3	398	341
#AS10	209	187
#AS12	233	254
Defective colonies		
#715	201	215
#719	179	193
#774	156	113
#784	103	117
#738	97	80

[0145]

5 [Effects of the Invention]

The presence of non-random mutations on human chromosome 1p in many malignant tumors was proposed by cytogenetic and molecular biological approaches. These facts suggest that one or more gene mutations on chromosome 1p are important for malignant tumors. As the human Gros1 gene of the present invention is present on the chromosome 1p region and has the activity to suppress tumors, this

gene may be a causative gene for these diseases. Therefore, the proteins or genes of the present invention, as well as a compound which promotes the activity of the proteins of the present invention can be used as useful tools for purifying and cloning novel factors involved in cell proliferation, and furthermore, can be used for developing pharmaceuticals for treating or preventing various tumors.

[0145]

[Sequence Listing]

10

SEQUENCE LISTING

<110> CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE, INC.

<120> Tumor suppressor genes

15

<130> C1-104

<140>

<141>

20

<160> 15

<170> PatentIn Ver. 2.0

25

<210> 1

<211> 2829

<212> DNA

<213> Homo sapiens

30

<220>

<221> CDS

<222> (52).. (1140)

<400> 1

35

ctccggcctt ggtggcgggt ggctggcgggt tccgttaggt ctgagggagc g atg gcg 57

Met Ala

1

	gta cgc gcg ttg aag ctg ctg acc aca ctg ctg gct gtc gtg gcc gct	105
	Val Arg Ala Leu Lys Leu Leu Thr Thr Leu Leu Ala Val Val Ala Ala	
5	5 10 15	
	gcc tcc caa gcc gag gtc gag tcc gag gca gga tgg ggc atg gtg acg	153
	Ala Ser Gln Ala Glu Val Glu Ser Glu Ala Gly Trp Gly Met Val Thr	
	20 25 30	
10		
	cct gat ctg ctc ttc gcc gag ggg acc gca gcc tac gcg cgc ggg gac	201
	Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg Gly Asp	
	35 40 45 50	
15	tgg ccc ggg gtg gtc ctg agc atg gaa cgg gcg ctg cgc tcc cgg gca	249
	Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser Arg Ala	
	55 60 65	
	gcc ctc cgc gcc ctt cgc ctg cgc tgc cgc acc cag tgt gcc gcc gac	297
20	Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala Ala Asp	
	70 75 80	
	ttc ccg tgg gag ctg gac ccc gac tgg tcc ccc agc ccg gcc cag gcc	345
	Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala Gln Ala	
25	85 90 95	
	tcg ggc gcc ggc gcc ctg cgc gac ctg agc ttc ttc ggg ggc ctt ctg	393
	Ser Gly Ala Gly Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly Leu Leu	
	100 105 110	
30		
	cgt cgc gct gcc tgc ctg cgc cgc tgc ctc ggg ccg ccg gcc gcc cac	441
	Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala Ala His	
	115 120 125 130	
35	tcg ctc agc gaa gag atg gag ctg gag ttc cgc aag cgg agc ccc tac	489
	Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser Pro Tyr	

	135	140	145	
	aac tac ctg cag gtc gcc tac ttc aag atc aac aag ttg gag aaa gct			537
	Asn Tyr Leu Gln Val Ala Tyr Phe Lys Ile Asn Lys Leu Glu Lys Ala			
5	150	155	160	
	gtt gct gca gca cac acc ttc ttc gtg ggc aat cct gag cac atg gaa			585
	Val Ala Ala Ala His Thr Phe Phe Val Gly Asn Pro Glu His Met Glu			
	165	170	175	
10	atg cag cag aac cta gac tat tac caa acc atg tct gga gtg aag gag			633
	Met Gln Gln Asn Leu Asp Tyr Tyr Gln Thr Met Ser Gly Val Lys Glu			
	180	185	190	
15	gcc gac ttc aag gat ctt gag act caa ccc cat atg caa gaa ttt cga			681
	Ala Asp Phe Lys Asp Leu Glu Thr Gln Pro His Met Gln Glu Phe Arg			
	195	200	205	210
	ctg gga gtg cga ctc tac tca gag gaa cag cca cag gaa gct gtg ccc			729
20	Leu Gly Val Arg Leu Tyr Ser Glu Glu Gln Pro Gln Glu Ala Val Pro			
	215	220	225	
	cac cta gag gcg gcg ctg caa gaa tac ttt gtg gcc tat gag gag tgc			777
	His Leu Glu Ala Ala Leu Gln Glu Tyr Phe Val Ala Tyr Glu Glu Cys			
25	230	235	240	
	cgt gcc ctc tgc gaa ggg ccc tat gac tac gat ggc tac aac tac ctt			825
	Arg Ala Leu Cys Glu Gly Pro Tyr Asp Tyr Asp Gly Tyr Asn Tyr Leu			
	245	250	255	
30	gag tac aac gct gac ctc ttc cag gcc atc aca gat cat tac atc cag			873
	Glu Tyr Asn Ala Asp Leu Phe Gln Ala Ile Thr Asp His Tyr Ile Gln			
	260	265	270	
35	gtc ctc aac tgt aag cag aac tgt gtc acg gag ctt gct tcc cac cca			921
	Val Leu Asn Cys Lys Gln Asn Cys Val Thr Glu Leu Ala Ser His Pro			

	275	280	285	290	
	agt cga gag aag ccc ttt gaa gac ttc ctc cca tcg cat tat aat tat				969
	Ser Arg Glu Lys Pro Phe Glu Asp Phe Leu Pro Ser His Tyr Asn Tyr				
5		295	300	305	
	ctg cag ttt gcc tac tat aac att ggg aat tat aca caa gct ggt gaa				1017
	Leu Gln Phe Ala Tyr Tyr Asn Ile Gly Asn Tyr Thr Gln Ala Gly Glu				
		310	315	320	
10					
	tgt gcc aag acc tat ctt ctc ttc ttc ccc aat gac gag gtg atg aac				1065
	Cys Ala Lys Thr Tyr Leu Leu Phe Phe Pro Asn Asp Glu Val Met Asn				
		325	330	335	
15					
	caa aat ttg gcc tat tat gca gct atg ctt gga gaa gaa cac acc aga				1113
	Gln Asn Leu Ala Tyr Tyr Ala Ala Met Leu Gly Glu Glu His Thr Arg				
		340	345	350	
	tcc atc ggc ccc cgt gag cag ggc acc tagggaaaga tgtgaccccg				1160
20	Ser Ile Gly Pro Arg Glu Gln Gly Thr				
		355	360		
	gaaagtactc agtttccctg ccctggagtg ccaaggagta ccgacagcga agcctactgg				1220
25					
	aaaaagaact gcttttcttc gcttatgatg tttttggaat tccctttgtg gatcgggatt				1280
	catggactcc agaagaaatg attcccaaga aattgcaaga gaaacagaag tgaggacctt				1340
	gaagaaactg catggttggg tcaagtctgat gaagcacttg aggcttcttg agcccaggca				1400
30					
	gatgtgaact cctggcaagg ggtgggcagg tccagtttgg gaagtcgggg tggagcccag				1460
	ggctggccct ggaatgcagt cctcagagcg gttgtgctca taggtcagaa cgggaaacag				1520
35					
	ccgtacgcat ctcccaggag attgggaacc ttatgaagga aatcgagacc cttgtggaag				1580

agaagaccaa ggagtcactg gatgtgagca gactgaccgc ggaaggtggc cccctgctgt 1640
 atgaaggcat cagtctcacc atgaactcca aactcctgaa tggttaccag cgggtggtga 1700
 5 tggacggcgt aatctctgac cacgagtgtc aggagctgca gagactgacc aatgtggcag 1760
 caacctcagg agatggctac cggggtcaga cctccccaca tactcccaat gaaaagttct 1820
 atggtgtcac tgtcttcaaa gccctcaagc tggggcaaga aggcaaagtt cctctgcaga 1880
 10 gtgccacact gtactacaac gtgacggaga aagtgcggcg catcatggag tcctacttcc 1940
 gcctggatac gccctctac ttttcctact ctcactgtgt gtgccgcact gccatcgaag 2000
 15 aggtccaggc agagaggaag gatgatagtc atccagtcca cgtggacaac tgcatcctga 2060
 atgccgagac cctcgtgtgt gtcaaagagc cccagccta caccttcgc gactacagcg 2120
 ccatccttta cctaaatggg gacttcgatg gcggaaactt ttatttcact gaactggatg 2180
 20 ccaagaccgt gacggcagag gtgcagcctc agtgtggaag agccgtggga ttctcttcag 2240
 gcactgaaaa cccacatgga gtgaaggctg tcaccagggg gcagcgtgtg gccatcgccc 2300
 25 tgtggttcac cctggaccct cgacacagcg agcgggacag ggtgcaggca gatgacctgg 2360
 tgaagatgct cttcagccca gaagagatgg acctctcca ggagcagccc ctggatgccc 2420
 agcagggecc cccgaacct gcacaagagt ctctctcagg cagtgaatcg aagcccaagg 2480
 30 atgagctatg acagcgtcca ggtcagacgg atgggtgact agacccatga agaggaactc 2540
 ttcttgcaat ctgagctggc cagccctcgc gggctgcaga gcagtgagcc tacatctgcc 2600
 35 actcagccga ggggaccctg ctcacagcct tctacatggt gctactgctc ttggagtgga 2660

catgaccaga caccgcaccc cctggatctg gctgagggct caggacacag gccagccac 2720

ccccaggggc ctccacagge cgctgcataa cagcgataca gtacttaagt gtctgtgtag 2780

5 acaaccaaag aataaatgat tcatggtttt ttttaaaaaa aaaaaaaaaa 2829

<210> 2

<211> 363

10 <212> PRT

<213> Homo sapiens

<400> 2

Met Ala Val Arg Ala Leu Lys Leu Leu Thr Thr Leu Leu Ala Val Val

15 1 5 10 15

Ala Ala Ala Ser Gln Ala Glu Val Glu Ser Glu Ala Gly Trp Gly Met

20 25 30

20 Val Thr Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg

35 40 45

Gly Asp Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser

50 55 60

25

Arg Ala Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala

65 70 75 80

Ala Asp Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala

30 85 90 95

Gln Ala Ser Gly Ala Gly Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly

100 105 110

35 Leu Leu Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala

115 120 125

	Ala His Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser	
	130	140
5	Pro Tyr Asn Tyr Leu Gln Val Ala Tyr Phe Lys Ile Asn Lys Leu Glu	
	145	160
	Lys Ala Val Ala Ala Ala His Thr Phe Phe Val Gly Asn Pro Glu His	
	165	175
10	Met Glu Met Gln Gln Asn Leu Asp Tyr Tyr Gln Thr Met Ser Gly Val	
	180	190
	Lys Glu Ala Asp Phe Lys Asp Leu Glu Thr Gln Pro His Met Gln Glu	
15	195	205
	Phe Arg Leu Gly Val Arg Leu Tyr Ser Glu Glu Gln Pro Gln Glu Ala	
	210	220
20	Val Pro His Leu Glu Ala Ala Leu Gln Glu Tyr Phe Val Ala Tyr Glu	
	225	240
	Glu Cys Arg Ala Leu Cys Glu Gly Pro Tyr Asp Tyr Asp Gly Tyr Asn	
	245	255
25	Tyr Leu Glu Tyr Asn Ala Asp Leu Phe Gln Ala Ile Thr Asp His Tyr	
	260	270
	Ile Gln Val Leu Asn Cys Lys Gln Asn Cys Val Thr Glu Leu Ala Ser	
30	275	285
	His Pro Ser Arg Glu Lys Pro Phe Glu Asp Phe Leu Pro Ser His Tyr	
	290	300
35	Asn Tyr Leu Gln Phe Ala Tyr Tyr Asn Ile Gly Asn Tyr Thr Gln Ala	
	305	320

cct gat ctg ctc ttc gcc gag ggg acc gca gcc tac gcg cgc ggg gac 201
Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg Gly Asp
35 40 45 50

	tgg ccc ggg gtg gtc ctg agc atg gaa cgg gcg ctg cgc tcc cgg gca	249
	Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser Arg Ala	
	55 60 65	
5	gcc ctc cgc gcc ctt cgc ctg cgc tgc cgc acc cag tgt gcc gcc gac	297
	Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala Ala Asp	
	70 75 80	
10	ttc ccg tgg gag ctg gac ccc gac tgg tcc ccc agc ccg gcc cag gcc	345
	Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala Gln Ala	
	85 90 95	
	tcg ggc gcc ggc gcc ctg cgc gac ctg agc ttc ttc ggg ggc ctt ctg	393
15	Ser Gly Ala Gly Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly Leu Leu	
	100 105 110	
	cgt cgc gct gcc tgc ctg cgc cgc tgc ctc ggg ccg ccg gcc gcc cac	441
	Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala Ala His	
20	115 120 125 130	
	tcg ctc agc gaa gag atg gag ctg gag ttc cgc aag cgg agc ccc tac	489
	Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser Pro Tyr	
	135 140 145	
25	aac tac ctg cag gtc gcc tac ttc aag atc aac aag ttg gag aaa gct	537
	Asn Tyr Leu Gln Val Ala Tyr Phe Lys Ile Asn Lys Leu Glu Lys Ala	
	150 155 160	
30	gtt gct gca gca cac acc ttc ttc gtg ggc aat cct gag cac atg gaa	585
	Val Ala Ala Ala His Thr Phe Phe Val Gly Asn Pro Glu His Met Glu	
	165 170 175	
	atg cag cag aac cta gac tat tac caa acc atg tct gga gtg aag gag	633
35	Met Gln Gln Asn Leu Asp Tyr Tyr Gln Thr Met Ser Gly Val Lys Glu	
	180 185 190	

gcc gac ttc aag gat ctt gag act caa ccc cat atg caa gaa ttt cga 681
 Ala Asp Phe Lys Asp Leu Glu Thr Gln Pro His Met Gln Glu Phe Arg
 195 200 205 210

5

ctg gga gtg cga ctc tac tca gag gaa cag cca cag gaa gct gtg ccc 729
 Leu Gly Val Arg Leu Tyr Ser Glu Glu Gln Pro Gln Glu Ala Val Pro
 215 220 225

10

cac cta gag gcg gcg ctg caa gaa tac ttt gtg gcc tat gag gag tgc 777
 His Leu Glu Ala Ala Leu Gln Glu Tyr Phe Val Ala Tyr Glu Glu Cys
 230 235 240

15

cgt gcc ctc tgc gaa ggg ccc tat gac tac gat ggc tac aac tac ctt 825
 Arg Ala Leu Cys Glu Gly Pro Tyr Asp Tyr Asp Gly Tyr Asn Tyr Leu
 245 250 255

20

gag tac aac gct gac ctc ttc cag gcc atc aca gat cat tac atc cag 873
 Glu Tyr Asn Ala Asp Leu Phe Gln Ala Ile Thr Asp His Tyr Ile Gln
 260 265 270

25

gtc ctc aac tgt aag cag aac tgt gtc acg gag ctt gct tcc cac cca 921
 Val Leu Asn Cys Lys Gln Asn Cys Val Thr Glu Leu Ala Ser His Pro
 275 280 285 290

30

agt cga gag aag ccc ttt gaa gac ttc ctc cca tcg cat tat aat tat 969
 Ser Arg Glu Lys Pro Phe Glu Asp Phe Leu Pro Ser His Tyr Asn Tyr
 295 300 305

35

ctg cag ttt gcc tac tat aac att ggg aat tat aca caa gct ggt gaa 1017
 Leu Gln Phe Ala Tyr Tyr Asn Ile Gly Asn Tyr Thr Gln Ala Gly Glu
 310 315 320

tgt gcc aag acc tat ctt ctc ttc ttc ccc aat gac gag gtg atg aac 1065
 Cys Ala Lys Thr Tyr Leu Leu Phe Phe Pro Asn Asp Glu Val Met Asn
 325 330 335

caa aat ttg gcc tat tat gca gct atg ctt gga gaa gaa cac acc aga 1113
 Gln Asn Leu Ala Tyr Tyr Ala Ala Met Leu Gly Glu Glu His Thr Arg
 340 345 350

5

tcc atc ggc ccc cgt gag agt gcc aag gag tac cga cag cga agc cta 1161
 Ser Ile Gly Pro Arg Glu Ser Ala Lys Glu Tyr Arg Gln Arg Ser Leu
 355 360 365 370

10

ctg gaa aaa gaa ctg ctt ttc ttc gct tat gat gtt ttt gga att ccc 1209
 Leu Glu Lys Glu Leu Leu Phe Phe Ala Tyr Asp Val Phe Gly Ile Pro
 375 380 385

15

ttt gtg gat ccg gat tca tgg act cca gaa gaa gtg att ccc aag aga 1257
 Phe Val Asp Pro Asp Ser Trp Thr Pro Glu Glu Val Ile Pro Lys Arg
 390 395 400

20

ttg caa gag aaa cag aag tca gaa cgg gaa aca gcc gta cgc atc tcc 1305
 Leu Gln Glu Lys Gln Lys Ser Glu Arg Glu Thr Ala Val Arg Ile Ser
 405 410 415

25

cag gag att ggg aac ctt atg aag gaa atc gag acc ctt gtg gaa gag 1353
 Gln Glu Ile Gly Asn Leu Met Lys Glu Ile Glu Thr Leu Val Glu Glu
 420 425 430

30

aag acc aag gag tca ctg gat gtg agc aga ctg acc cgg gaa ggt ggc 1401
 Lys Thr Lys Glu Ser Leu Asp Val Ser Arg Leu Thr Arg Glu Gly Gly
 435 440 445 450

35

ccc ctg ctg tat gaa ggc atc agt ctc acc atg aac tcc aaa ctc ctg 1449
 Pro Leu Leu Tyr Glu Gly Ile Ser Leu Thr Met Asn Ser Lys Leu Leu
 455 460 465

aat ggt tac cag cgg gtg gtg atg gac ggc gta atc tct gac cac gag 1497
 Asn Gly Tyr Gln Arg Val Val Met Asp Gly Val Ile Ser Asp His Glu
 470 475 480

	tgt cag gag ctg cag aga ctg acc aat gtg gca gca acc tca gga gat	1545
	Cys Gln Glu Leu Gln Arg Leu Thr Asn Val Ala Ala Thr Ser Gly Asp	
	485 490 495	
5	ggc tac cgg ggt cag acc tcc cca cat act ccc aat gaa aag ttc tat	1593
	Gly Tyr Arg Gly Gln Thr Ser Pro His Thr Pro Asn Glu Lys Phe Tyr	
	500 505 510	
10	ggc gtc act gtc ttc aaa gcc ctc aag ctg ggg caa gaa ggc aaa gtt	1641
	Gly Val Thr Val Phe Lys Ala Leu Lys Leu Gly Gln Glu Gly Lys Val	
	515 520 525 530	
	cct ctg cag agt gcc cac ctg tac tac aac gtg acg gag aaa gtg cgg	1689
15	Pro Leu Gln Ser Ala His Leu Tyr Tyr Asn Val Thr Glu Lys Val Arg	
	535 540 545	
	cgc atc atg gag tcc tac ttc cgc ctg gat acg ccc ctc tac ttt tcc	1737
	Arg Ile Met Glu Ser Tyr Phe Arg Leu Asp Thr Pro Leu Tyr Phe Ser	
20	550 555 560	
	tac tct cat ctg gtg tgc cgc act gcc atc gaa gag gtc cag gca gag	1785
	Tyr Ser His Leu Val Cys Arg Thr Ala Ile Glu Glu Val Gln Ala Glu	
	565 570 575	
25	agg aag gat gat agt cat cca gtc cac gtg gac aac tgc atc ctg aat	1833
	Arg Lys Asp Asp Ser His Pro Val His Val Asp Asn Cys Ile Leu Asn	
	580 585 590	
30	gcc gag acc ctc gtg tgt gtc aaa gag ccc cca gcc tac acc ttc cgc	1881
	Ala Glu Thr Leu Val Cys Val Lys Glu Pro Pro Ala Tyr Thr Phe Arg	
	595 600 605 610	
	gac tac agc gcc atc ctt tac cta aat ggg gac ttc gat ggc gga aac	1929
35	Asp Tyr Ser Ala Ile Leu Tyr Leu Asn Gly Asp Phe Asp Gly Gly Asn	
	615 620 625	

ttt tat ttc act gaa ctg gat gcc aag acc gtg acg gca gag gtg cag 1977
 Phe Tyr Phe Thr Glu Leu Asp Ala Lys Thr Val Thr Ala Glu Val Gln
 630 635 640

5

cct cag tgt gga aga gcc gtg gga ttc tct tca ggc act gaa aac cca 2025
 Pro Gln Cys Gly Arg Ala Val Gly Phe Ser Ser Gly Thr Glu Asn Pro
 645 650 655

10

cat gga gtg aag gct gtc acc agg ggg cag cgc tgt gcc atc gcc ctg 2073
 His Gly Val Lys Ala Val Thr Arg Gly Gln Arg Cys Ala Ile Ala Leu
 660 665 670

15

tgg ttc acc ctg gac cct cga cac agc gag cgg gac agg gtg cag gca 2121
 Trp Phe Thr Leu Asp Pro Arg His Ser Glu Arg Asp Arg Val Gln Ala
 675 680 685 690

20

gat gac ctg gtg aag atg ctc ttc agc cca gaa gag atg gac ctc tcc 2169
 Asp Asp Leu Val Lys Met Leu Phe Ser Pro Glu Glu Met Asp Leu Ser
 695 700 705

25

cag gag cag ccc ctg gat gcc cag cag ggc ccc ccc gaa cct gca caa 2217
 Gln Glu Gln Pro Leu Asp Ala Gln Gln Gly Pro Pro Glu Pro Ala Gln
 710 715 720

30

gag tct ctc tca ggc agt gaa tcg aag ccc aag gat gag cta 2259
 Glu Ser Leu Ser Gly Ser Glu Ser Lys Pro Lys Asp Glu Leu
 725 730 735

35

tgacagcgtc caggtcagac ggatgggtga ctagacccat gaagaggaac tcttcttgca 2319
 ctctgagctg gccagcccct cggggctgca gagcagtgag cctacatctg ccactcagcc 2379
 gaggggaccc tgctcacagc cttctacatg gtgctactgc tcttggagtg gacatgacca 2439
 gacaccgcac cccctggatc tggctgaggg ctcaggacac aggcccagcc acccccaggg 2499

gcctccacag gccgctgcat aacagcgata cagtacttaa gtgtctgtgt agacaaccaa 2559

agaataaatg attcatgggt ttttttaaaa aaaaaaaaaa a 2600

5

<210> 4

<211> 736

<212> PRT

10 <213> Homo sapiens

<400> 4

Met Ala Val Arg Ala Leu Lys Leu Leu Thr Thr Leu Leu Ala Val Val

1 5 10 15

15

Ala Ala Ala Ser Gln Ala Glu Val Glu Ser Glu Ala Gly Trp Gly Met

20 25 30

Val Thr Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg

20 35 40 45

Gly Asp Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser

50 55 60

25 Arg Ala Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala

65 70 75 80

Ala Asp Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala

85 90 95

30

Gln Ala Ser Gly Ala Gly Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly

100 105 110

Leu Leu Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala

35 115 120 125

	Ala His Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser	
	130	135 140
5	Pro Tyr Asn Tyr Leu Gln Val Ala Tyr Phe Lys Ile Asn Lys Leu Glu	
	145	150 155 160
	Lys Ala Val Ala Ala Ala His Thr Phe Phe Val Gly Asn Pro Glu His	
		165 170 175
10	Met Glu Met Gln Gln Asn Leu Asp Tyr Tyr Gln Thr Met Ser Gly Val	
		180 185 190
	Lys Glu Ala Asp Phe Lys Asp Leu Glu Thr Gln Pro His Met Gln Glu	
		195 200 205
15	Phe Arg Leu Gly Val Arg Leu Tyr Ser Glu Glu Gln Pro Gln Glu Ala	
		210 215 220
	Val Pro His Leu Glu Ala Ala Leu Gln Glu Tyr Phe Val Ala Tyr Glu	
20		225 230 235 240
	Glu Cys Arg Ala Leu Cys Glu Gly Pro Tyr Asp Tyr Asp Gly Tyr Asn	
		245 250 255
25	Tyr Leu Glu Tyr Asn Ala Asp Leu Phe Gln Ala Ile Thr Asp His Tyr	
		260 265 270
	Ile Gln Val Leu Asn Cys Lys Gln Asn Cys Val Thr Glu Leu Ala Ser	
		275 280 285
30	His Pro Ser Arg Glu Lys Pro Phe Glu Asp Phe Leu Pro Ser His Tyr	
		290 295 300
	Asn Tyr Leu Gln Phe Ala Tyr Tyr Asn Ile Gly Asn Tyr Thr Gln Ala	
35		305 310 315 320

	Gly	Glu	Cys	Ala	Lys	Thr	Tyr	Leu	Leu	Phe	Phe	Pro	Asn	Asp	Glu	Val	
					325					330					335		
	Met	Asn	Gln	Asn	Leu	Ala	Tyr	Tyr	Ala	Ala	Met	Leu	Gly	Glu	Glu	His	
5				340					345					350			
	Thr	Arg	Ser	Ile	Gly	Pro	Arg	Glu	Ser	Ala	Lys	Glu	Tyr	Arg	Gln	Arg	
				355				360					365				
10	Ser	Leu	Leu	Glu	Lys	Glu	Leu	Leu	Phe	Phe	Ala	Tyr	Asp	Val	Phe	Gly	
		370				375					380						
	Ile	Pro	Phe	Val	Asp	Pro	Asp	Ser	Trp	Thr	Pro	Glu	Glu	Val	Ile	Pro	
	385					390				395					400		
15	Lys	Arg	Leu	Gln	Glu	Lys	Gln	Lys	Ser	Glu	Arg	Glu	Thr	Ala	Val	Arg	
				405					410					415			
	Ile	Ser	Gln	Glu	Ile	Gly	Asn	Leu	Met	Lys	Glu	Ile	Glu	Thr	Leu	Val	
20			420					425					430				
	Glu	Glu	Lys	Thr	Lys	Glu	Ser	Leu	Asp	Val	Ser	Arg	Leu	Thr	Arg	Glu	
			435					440					445				
25	Gly	Gly	Pro	Leu	Leu	Tyr	Glu	Gly	Ile	Ser	Leu	Thr	Met	Asn	Ser	Lys	
		450				455					460						
	Leu	Leu	Asn	Gly	Tyr	Gln	Arg	Val	Val	Met	Asp	Gly	Val	Ile	Ser	Asp	
	465				470					475				480			
30	His	Glu	Cys	Gln	Glu	Leu	Gln	Arg	Leu	Thr	Asn	Val	Ala	Ala	Thr	Ser	
				485					490					495			
	Gly	Asp	Gly	Tyr	Arg	Gly	Gln	Thr	Ser	Pro	His	Thr	Pro	Asn	Glu	Lys	
35			500					505					510				

	Phe Tyr Gly Val Thr Val Phe Lys Ala Leu Lys Leu Gly Gln Glu Gly	
	515	520 525
5	Lys Val Pro Leu Gln Ser Ala His Leu Tyr Tyr Asn Val Thr Glu Lys	
	530	535 540
	Val Arg Arg Ile Met Glu Ser Tyr Phe Arg Leu Asp Thr Pro Leu Tyr	
	545	550 555 560
10	Phe Ser Tyr Ser His Leu Val Cys Arg Thr Ala Ile Glu Glu Val Gln	
	565	570 575
	Ala Glu Arg Lys Asp Asp Ser His Pro Val His Val Asp Asn Cys Ile	
	580	585 590
15	Leu Asn Ala Glu Thr Leu Val Cys Val Lys Glu Pro Pro Ala Tyr Thr	
	595	600 605
	Phe Arg Asp Tyr Ser Ala Ile Leu Tyr Leu Asn Gly Asp Phe Asp Gly	
20	610	615 620
	Gly Asn Phe Tyr Phe Thr Glu Leu Asp Ala Lys Thr Val Thr Ala Glu	
	625	630 635 640
25	Val Gln Pro Gln Cys Gly Arg Ala Val Gly Phe Ser Ser Gly Thr Glu	
	645	650 655
	Asn Pro His Gly Val Lys Ala Val Thr Arg Gly Gln Arg Cys Ala Ile	
	660	665 670
30	Ala Leu Trp Phe Thr Leu Asp Pro Arg His Ser Glu Arg Asp Arg Val	
	675	680 685
	Gln Ala Asp Asp Leu Val Lys Met Leu Phe Ser Pro Glu Glu Met Asp	
35	690	695 700

Leu Ser Gln Glu Gln Pro Leu Asp Ala Gln Gln Gly Pro Pro Glu Pro
 705 710 715 720

Ala Gln Glu Ser Leu Ser Gly Ser Glu Ser Lys Pro Lys Asp Glu Leu
 5 725 730 735

<210> 5

<211> 2416

10 <212> DNA

<213> Mus musculus

<220>

<221> CDS

15 <222> (12).. (2252)

<400> 5

ggagcaaggc c atg gcg gtg acg aaa gga ggc tgc tgg cac gat gct agc 50
 Met Ala Val Thr Lys Gly Gly Cys Trp His Asp Ala Ser

20 1 5 10

ggt cgc cgc cgc cgc cgc ctt acg ggt tgc ggc gag tct gag ccg gga 98
 Gly Arg Arg Arg Arg Arg Leu Thr Gly Cys Gly Glu Ser Glu Pro Gly
 15 20 25

25

tgg gac gtg gca gcc cct gac ctg ctt tac gca gag ggg acc gcg gcc 146
 Trp Asp Val Ala Ala Pro Asp Leu Leu Tyr Ala Glu Gly Thr Ala Ala
 30 35 40 45

30

tac tcg cgc agg gac tgg ccc ggg gtg gtc ctg aac atg gag cgg gct 194
 Tyr Ser Arg Arg Asp Trp Pro Gly Val Val Leu Asn Met Glu Arg Ala
 50 55 60

ctg cgc tcg cgg gcg gcc ctg cgt gcc ctc cgc ctg cgc tgc cgc aca 242

35 Leu Arg Ser Arg Ala Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr
 65 70 75

cgc tgt gcc acc gaa ctg ccg tgg gca ccg gac ctg gat ctc ggt ccg 290
 Arg Cys Ala Thr Glu Leu Pro Trp Ala Pro Asp Leu Asp Leu Gly Pro
 80 85 90

5

gac ccc agc ctg agc cag gac ccg ggc gcc gcc gcc ctg cac gac ctg 338
 Asp Pro Ser Leu Ser Gln Asp Pro Gly Ala Ala Ala Leu His Asp Leu
 95 100 105

10

cgc ttc ttc gga gcc gtg ctg cgc cgt gcc gcc tgc cta cgc cgc tgc 386
 Arg Phe Phe Gly Ala Val Leu Arg Arg Ala Ala Cys Leu Arg Arg Cys
 110 115 120 125

15

ctc ggg ccg ccc tct gcc cac ttg ctg agt gaa gaa ctg gac ctg gag 434
 Leu Gly Pro Pro Ser Ala His Leu Leu Ser Glu Glu Leu Asp Leu Glu
 130 135 140

20

ttc aac aag cgg agc ccg tac aac tac ctg cag gtc gcc tat ttc aag 482
 Phe Asn Lys Arg Ser Pro Tyr Asn Tyr Leu Gln Val Ala Tyr Phe Lys
 145 150 155

25

ata aac aag ctg gag aaa gct gtg gct gcg gca cac acc ttc ttt gtg 530
 Ile Asn Lys Leu Glu Lys Ala Val Ala Ala Ala His Thr Phe Phe Val
 160 165 170

30

ggc aat cct gag cac atg gag atg cgg cag aac ctc gac tat tac caa 578
 Gly Asn Pro Glu His Met Glu Met Arg Gln Asn Leu Asp Tyr Tyr Gln
 175 180 185

35

acc atg tct ggg gtg aag gag gca gac ttc agg gat ctc gag gcc aag 626
 Thr Met Ser Gly Val Lys Glu Ala Asp Phe Arg Asp Leu Glu Ala Lys
 190 195 200 205

ccc cat atg cat gag ttt cgg ctg ggg gta cga ctc tac tca gag gag 674
 Pro His Met His Glu Phe Arg Leu Gly Val Arg Leu Tyr Ser Glu Glu
 210 215 220

	aag cca cag gaa gct gtg ccc cac ctg gag gcg gca ctg caa gag tac	722
	Lys Pro Gln Glu Ala Val Pro His Leu Glu Ala Ala Leu Gln Glu Tyr	
	225 230 235	
5	ttt gtg gcc gat gag gag tgc cgt gcc ctc tgc gaa ggg ccc tat gac	770
	Phe Val Ala Asp Glu Glu Cys Arg Ala Leu Cys Glu Gly Pro Tyr Asp	
	240 245 250	
10	tac gac ggc tac aac tac cta gac tac agc gct gac ctc ttc cag gcc	818
	Tyr Asp Gly Tyr Asn Tyr Leu Asp Tyr Ser Ala Asp Leu Phe Gln Ala	
	255 260 265	
	atc aca gat cat tac gtc cag gtc ctc aac tgt aag cag aac tgt gtc	866
15	Ile Thr Asp His Tyr Val Gln Val Leu Asn Cys Lys Gln Asn Cys Val	
	270 275 280 285	
	acg gag ctg gct tcc cac cca agt agg gaa aag ccc ttt gaa gac ttc	914
	Thr Glu Leu Ala Ser His Pro Ser Arg Glu Lys Pro Phe Glu Asp Phe	
20	290 295 300	
	ctc cct tca cac tat aat tac cta cag ttt gcc tac tac aac att ggg	962
	Leu Pro Ser His Tyr Asn Tyr Leu Gln Phe Ala Tyr Tyr Asn Ile Gly	
	305 310 315	
25	aac tat aca caa gct att gaa tgt gcc aag acc tac ctc ctc ttc ttt	1010
	Asn Tyr Thr Gln Ala Ile Glu Cys Ala Lys Thr Tyr Leu Leu Phe Phe	
	320 325 330	
30	ccc aat gat gag gtg atg cac cag aat ctg gct tat tac aca gcc atg	1058
	Pro Asn Asp Glu Val Met His Gln Asn Leu Ala Tyr Tyr Thr Ala Met	
	335 340 345	
	ctt gga gaa gaa gag gcc agc tcc atc agc ccc agg gag aat gcc gag	1106
35	Leu Gly Glu Glu Glu Ala Ser Ser Ile Ser Pro Arg Glu Asn Ala Glu	
	350 355 360 365	

	gaa tac cga cgt cca aac ctg ttg gag aaa gaa ctg ctt ttc ttc gct	1154
	Glu Tyr Arg Arg Pro Asn Leu Leu Glu Lys Glu Leu Leu Phe Phe Ala	
	370 375 380	
5	tat gac att ttt gga att ccc ttt gtg gat ccc gat tca tgg act cca	1202
	Tyr Asp Ile Phe Gly Ile Pro Phe Val Asp Pro Asp Ser Trp Thr Pro	
	385 390 395	
10	gaa gaa gtg att ccc aag aga ttg caa gag aaa cag aag tct gaa cgg	1250
	Glu Glu Val Ile Pro Lys Arg Leu Gln Glu Lys Gln Lys Ser Glu Arg	
	400 405 410	
	gaa aca gcc gta cgc atc tcc cag gag att ggg aac ctt atg aag gaa	1298
15	Glu Thr Ala Val Arg Ile Ser Gln Glu Ile Gly Asn Leu Met Lys Glu	
	415 420 425	
	atc gag acc ctt gtg gaa gag aag acc aag gag tct ctg gat gtg agc	1346
	Ile Glu Thr Leu Val Glu Glu Lys Thr Lys Glu Ser Leu Asp Val Ser	
20	430 435 440 445	
	aga ctg acc cgg gaa ggt ggt ccc ctg ctg tat gaa ggc atc agt ctc	1394
	Arg Leu Thr Arg Glu Gly Gly Pro Leu Leu Tyr Glu Gly Ile Ser Leu	
	450 455 460	
25	acc atg aac tcc aaa gtc ttg aat ggc tcc cag cgg gtg gtg atg gat	1442
	Thr Met Asn Ser Lys Val Leu Asn Gly Ser Gln Arg Val Val Met Asp	
	465 470 475	
30	ggt gtg atc tct gat gat gag tgc cag gag ctg cag aga ctg acc aat	1490
	Gly Val Ile Ser Asp Asp Glu Cys Gln Glu Leu Gln Arg Leu Thr Asn	
	480 485 490	
	gcg gca gca act tcg gga gat ggc tac cga ggt cag acc tcc cca cac	1538
35	Ala Ala Ala Thr Ser Gly Asp Gly Tyr Arg Gly Gln Thr Ser Pro His	
	495 500 505	

	acc	cca	aat	gaa	aag	ttc	tat	ggt	gtt	act	gtc	ctc	aaa	gct	ctc	aag	1586
	Thr	Pro	Asn	Glu	Lys	Phe	Tyr	Gly	Val	Thr	Val	Leu	Lys	Ala	Leu	Lys	
	510					515					520					525	
5																	
	ctc	ggg	cag	gaa	gga	aaa	gtt	cct	ctg	cag	agt	gcc	cgc	atg	tac	tac	1634
	Leu	Gly	Gln	Glu	Gly	Lys	Val	Pro	Leu	Gln	Ser	Ala	Arg	Met	Tyr	Tyr	
					530					535					540		
10																	
	aac	gtg	aca	gag	aag	gtg	cgg	cgc	gtc	atg	gag	tcc	tac	ttc	cgc	ctg	1682
	Asn	Val	Thr	Glu	Lys	Val	Arg	Arg	Val	Met	Glu	Ser	Tyr	Phe	Arg	Leu	
				545					550					555			
15																	
	gac	acg	ccc	ctc	tat	ttc	tct	tat	tcc	cac	ttc	gtg	tgc	cgc	act	gca	1730
	Asp	Thr	Pro	Leu	Tyr	Phe	Ser	Tyr	Ser	His	Phe	Val	Cys	Arg	Thr	Ala	
				560					565					570			
20																	
	ata	gaa	gag	tca	cag	gct	gag	agg	aag	gac	agt	agc	cac	ccc	gtc	cac	1778
	Ile	Glu	Glu	Ser	Gln	Ala	Glu	Arg	Lys	Asp	Ser	Ser	His	Pro	Val	His	
		575					580						585				
25																	
	gtg	gat	aac	tgc	atc	ctg	aat	gcc	gaa	gcc	ttc	atg	tgt	atc	aag	gag	1826
	Val	Asp	Asn	Cys	Ile	Leu	Asn	Ala	Glu	Ala	Phe	Met	Cys	Ile	Lys	Glu	
	590					595					600					605	
30																	
	ccc	cca	gca	tac	acg	ttc	cgg	gaa	tac	agc	gcc	atc	ctt	tac	ctc	aat	1874
	Pro	Pro	Ala	Tyr	Thr	Phe	Arg	Glu	Tyr	Ser	Ala	Ile	Leu	Tyr	Leu	Asn	
					610					615					620		
35																	
	ggc	gac	ttc	gat	gga	gga	aac	ttt	tac	ttc	aca	gaa	cta	gat	gcc	aag	1922
	Gly	Asp	Phe	Asp	Gly	Gly	Asn	Phe	Tyr	Phe	Thr	Glu	Leu	Asp	Ala	Lys	
				625					630					635			
40																	
	act	gtg	acg	gca	gag	gtg	cag	ccc	cag	tgt	gga	agg	gct	gtg	gga	ttc	1970
	Thr	Val	Thr	Ala	Glu	Val	Gln	Pro	Gln	Cys	Gly	Arg	Ala	Val	Gly	Phe	
				640					645					650			

tct tct ggc act gag aac cca cat gga gtg aag gct gtc acc agg ggg 2018
 Ser Ser Gly Thr Glu Asn Pro His Gly Val Lys Ala Val Thr Arg Gly
 655 660 665

5

cag cgc tgc gcc atc gcc ctg tgg ttc acg ctg gat cct cgg cac agt 2066
 Gln Arg Cys Ala Ile Ala Leu Trp Phe Thr Leu Asp Pro Arg His Ser
 670 675 680 685

10

gag aga gac agg gtg cag gca gat gac ctg gtg aag atg ctg ttc agc 2114
 Glu Arg Asp Arg Val Gln Ala Asp Asp Leu Val Lys Met Leu Phe Ser
 690 695 700

15

cca gaa gag gtg gac ctc ccc cag gaa cag ccc ctg cct gac cag cag 2162
 Pro Glu Glu Val Asp Leu Pro Gln Glu Gln Pro Leu Pro Asp Gln Gln
 705 710 715

20

ggt tgc cca gag cct gga gaa gag ttt ctg cat ggt gct act gtt ctt 2210
 Gly Ser Pro Glu Pro Gly Glu Glu Phe Leu His Gly Ala Thr Val Leu
 720 725 730

25

gga gtg ggc ata gca gga cac act ctt ctc tgg gct tgg ctg 2252
 Gly Val Gly Ile Ala Gly His Thr Leu Leu Trp Ala Trp Leu
 735 740 745

taggctcaga atgcaggccc agaaccaccc tggggcctat gtaggcagct gccgtcagca 2312
 gcgtgatata ttttaagtgtc tgtaaagaca accaaagaat aaatgatttg tgtttttaaa 2372

30

aagnaiaaaaa aaaaaaaaaat taaaaatttg cgcggccgca agaa 2416

<210> 6

<211> 747

35 <212> PRT

<213> Mus musculus

<400> 6

	Met	Ala	Val	Thr	Lys	Gly	Gly	Cys	Trp	His	Asp	Ala	Ser	Gly	Arg	Arg
	1				5					10					15	
5	Arg	Arg	Arg	Leu	Thr	Gly	Cys	Gly	Glu	Ser	Glu	Pro	Gly	Trp	Asp	Val
				20					25					30		
	Ala	Ala	Pro	Asp	Leu	Leu	Tyr	Ala	Glu	Gly	Thr	Ala	Ala	Tyr	Ser	Arg
10			35					40						45		
	Arg	Asp	Trp	Pro	Gly	Val	Val	Leu	Asn	Met	Glu	Arg	Ala	Leu	Arg	Ser
		50					55					60				
15	Arg	Ala	Ala	Leu	Arg	Ala	Leu	Arg	Leu	Arg	Cys	Arg	Thr	Arg	Cys	Ala
	65					70					75				80	
	Thr	Glu	Leu	Pro	Trp	Ala	Pro	Asp	Leu	Asp	Leu	Gly	Pro	Asp	Pro	Ser
					85					90					95	
20	Leu	Ser	Gln	Asp	Pro	Gly	Ala	Ala	Ala	Leu	His	Asp	Leu	Arg	Phe	Phe
				100						105				110		
	Gly	Ala	Val	Leu	Arg	Arg	Ala	Ala	Cys	Leu	Arg	Arg	Cys	Leu	Gly	Pro
25			115					120					125			
	Pro	Ser	Ala	His	Leu	Leu	Ser	Glu	Glu	Leu	Asp	Leu	Glu	Phe	Asn	Lys
		130					135					140				
30	Arg	Ser	Pro	Tyr	Asn	Tyr	Leu	Gln	Val	Ala	Tyr	Phe	Lys	Ile	Asn	Lys
	145					150					155				160	
	Leu	Glu	Lys	Ala	Val	Ala	Ala	Ala	His	Thr	Phe	Phe	Val	Gly	Asn	Pro
				165					170					175		
35	Glu	His	Met	Glu	Met	Arg	Gln	Asn	Leu	Asp	Tyr	Tyr	Gln	Thr	Met	Ser

	180	185	190
	Gly Val Lys Glu Ala Asp Phe Arg Asp Leu Glu Ala Lys Pro His Met		
	195	200	205
5	His Glu Phe Arg Leu Gly Val Arg Leu Tyr Ser Glu Glu Lys Pro Gln		
	210	215	220
	Glu Ala Val Pro His Leu Glu Ala Ala Leu Gln Glu Tyr Phe Val Ala		
10	225	230	235 240
	Asp Glu Glu Cys Arg Ala Leu Cys Glu Gly Pro Tyr Asp Tyr Asp Gly		
	245	250	255
15	Tyr Asn Tyr Leu Asp Tyr Ser Ala Asp Leu Phe Gln Ala Ile Thr Asp		
	260	265	270
	His Tyr Val Gln Val Leu Asn Cys Lys Gln Asn Cys Val Thr Glu Leu		
	275	280	285
20	Ala Ser His Pro Ser Arg Glu Lys Pro Phe Glu Asp Phe Leu Pro Ser		
	290	295	300
	His Tyr Asn Tyr Leu Gln Phe Ala Tyr Tyr Asn Ile Gly Asn Tyr Thr		
25	305	310	315 320
	Gln Ala Ile Glu Cys Ala Lys Thr Tyr Leu Leu Phe Phe Pro Asn Asp		
	325	330	335
30	Glu Val Met His Gln Asn Leu Ala Tyr Tyr Thr Ala Met Leu Gly Glu		
	340	345	350
	Glu Glu Ala Ser Ser Ile Ser Pro Arg Glu Asn Ala Glu Glu Tyr Arg		
	355	360	365
35	Arg Pro Asn Leu Leu Glu Lys Glu Leu Leu Phe Phe Ala Tyr Asp Ile		

	370		375		380	
	Phe Gly Ile Pro Phe Val Asp Pro Asp Ser Trp Thr Pro Glu Glu Val					
	385		390		395	400
5	Ile Pro Lys Arg Leu Gln Glu Lys Gln Lys Ser Glu Arg Glu Thr Ala					
		405		410		415
	Val Arg Ile Ser Gln Glu Ile Gly Asn Leu Met Lys Glu Ile Glu Thr					
10		420		425		430
	Leu Val Glu Glu Lys Thr Lys Glu Ser Leu Asp Val Ser Arg Leu Thr					
		435		440		445
15	Arg Glu Gly Gly Pro Leu Leu Tyr Glu Gly Ile Ser Leu Thr Met Asn					
		450		455		460
	Ser Lys Val Leu Asn Gly Ser Gln Arg Val Val Met Asp Gly Val Ile					
		465		470		475
20	Ser Asp Asp Glu Cys Gln Glu Leu Gln Arg Leu Thr Asn Ala Ala Ala					
		485		490		495
	Thr Ser Gly Asp Gly Tyr Arg Gly Gln Thr Ser Pro His Thr Pro Asn					
25		500		505		510
	Glu Lys Phe Tyr Gly Val Thr Val Leu Lys Ala Leu Lys Leu Gly Gln					
		515		520		525
30	Glu Gly Lys Val Pro Leu Gln Ser Ala Arg Met Tyr Tyr Asn Val Thr					
		530		535		540
	Glu Lys Val Arg Arg Val Met Glu Ser Tyr Phe Arg Leu Asp Thr Pro					
		545		550		555
35	Leu Tyr Phe Ser Tyr Ser His Phe Val Cys Arg Thr Ala Ile Glu Glu					

	565	570	575
	Ser Gln Ala Glu Arg Lys Asp Ser Ser His Pro Val His Val Asp Asn		
	580	585	590
5	Cys Ile Leu Asn Ala Glu Ala Phe Met Cys Ile Lys Glu Pro Pro Ala		
	595	600	605
	Tyr Thr Phe Arg Glu Tyr Ser Ala Ile Leu Tyr Leu Asn Gly Asp Phe		
10	610	615	620
	Asp Gly Gly Asn Phe Tyr Phe Thr Glu Leu Asp Ala Lys Thr Val Thr		
	625	630	635 640
15	Ala Glu Val Gln Pro Gln Cys Gly Arg Ala Val Gly Phe Ser Ser Gly		
	645	650	655
	Thr Glu Asn Pro His Gly Val Lys Ala Val Thr Arg Gly Gln Arg Cys		
	660	665	670
20	Ala Ile Ala Leu Trp Phe Thr Leu Asp Pro Arg His Ser Glu Arg Asp		
	675	680	685
	Arg Val Gln Ala Asp Asp Leu Val Lys Met Leu Phe Ser Pro Glu Glu		
25	690	695	700
	Val Asp Leu Pro Gln Glu Gln Pro Leu Pro Asp Gln Gln Gly Ser Pro		
	705	710	715 720
30	Glu Pro Gly Glu Glu Phe Leu His Gly Ala Thr Val Leu Gly Val Gly		
	725	730	735
	Ile Ala Gly His Thr Leu Leu Trp Ala Trp Leu		
	740	745	

<210> 7
 <211> 2322
 <212> DNA
 <213> Mus musculus

5

<220>
 <221> CDS
 <222> (12).. (1637)

10 <400> 7

ggagcaaggc c atg gcg gtg acg aaa gga ggc tgc tgg cac gat gct agc 50

Met Ala Val Thr Lys Gly Gly Cys Trp His Asp Ala Ser

1

5

10

15 ggt cgc cgc cgc cgc cgc ctt acg ggt tgc ggc gag tct gag ccg gga 98

Gly Arg Arg Arg Arg Arg Leu Thr Gly Cys Gly Glu Ser Glu Pro Gly

15

20

25

tgg gac gtg gca gcc cct gac ctg ctt tac gca gag ggg acc gcg gcc 146

20 Trp Asp Val Ala Ala Pro Asp Leu Leu Tyr Ala Glu Gly Thr Ala Ala

30

35

40

45

tac tcg cgc agg gac tgg ccc ggg gtg gtc ctg aac atg gag cgg gct 194

Tyr Ser Arg Arg Asp Trp Pro Gly Val Val Leu Asn Met Glu Arg Ala

25

50

55

60

ctg cgc tcg cgg gcg gcc ctg cgt gcc ctc cgc ctg cgc tgc cgc aca 242

Leu Arg Ser Arg Ala Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr

65

70

75

30

cgc tgt gcc acc gaa ctg ccg tgg gca ccg gac ctg gat ctc ggt ccg 290

Arg Cys Ala Thr Glu Leu Pro Trp Ala Pro Asp Leu Asp Leu Gly Pro

80

85

90

35 gac ccc agc ctg agc cag gac ccg ggc gcc gcc gcc ctg cac gac ctg 338

Asp Pro Ser Leu Ser Gln Asp Pro Gly Ala Ala Ala Leu His Asp Leu

	95	100	105	
	cgc ttc ttc gga gcc gtg ctg cgc cgt gcc gcc tgc cta cgc cgc tgc	386		
	Arg Phe Phe Gly Ala Val Leu Arg Arg Ala Ala Cys Leu Arg Arg Cys			
5	110	115	120	125
	ctc ggg ccg ccc tct gcc cac ttg ctg agt gaa gaa ctg gac ctg gag	434		
	Leu Gly Pro Pro Ser Ala His Leu Leu Ser Glu Glu Leu Asp Leu Glu			
	130	135	140	
10	ttc aac aag cgg agc ccg tac aac tac ctg cag gtc gcc tat ttc aag	482		
	Phe Asn Lys Arg Ser Pro Tyr Asn Tyr Leu Gln Val Ala Tyr Phe Lys			
	145	150	155	
15	ata aac aag ctg gag aaa gct gtg gct gcg gca cac acc ttc ttt gtg	530		
	Ile Asn Lys Leu Glu Lys Ala Val Ala Ala Ala His Thr Phe Phe Val			
	160	165	170	
	ggc aat cct gag cac atg gag atg cgg cag aac ctc gac tat tac caa	578		
20	Gly Asn Pro Glu His Met Glu Met Arg Gln Asn Leu Asp Tyr Tyr Gln			
	175	180	185	
	acc atg tct ggg gtg aag gag gca gac ttc agg gat ctc gag gcc aag	626		
	Thr Met Ser Gly Val Lys Glu Ala Asp Phe Arg Asp Leu Glu Ala Lys			
25	190	195	200	205
	ccc cat atg cat gag ttt cgg ctg ggg gta cga ctc tac tca gag gag	674		
	Pro His Met His Glu Phe Arg Leu Gly Val Arg Leu Tyr Ser Glu Glu			
	210	215	220	
30	aag cca cag gaa gct gtg ccc cac ctg gag gcg gca ctg caa gag tac	722		
	Lys Pro Gln Glu Ala Val Pro His Leu Glu Ala Ala Leu Gln Glu Tyr			
	225	230	235	
35	ttt gtg gcc gat gag gag tgc cgt gcc ctc tgc gaa ggg ccc tat gac	770		
	Phe Val Ala Asp Glu Glu Cys Arg Ala Leu Cys Glu Gly Pro Tyr Asp			

	240	245	250	
	tac gac ggc tac aac tac cta gac tac agc gct gac ctc ttc cag gcc			818
	Tyr Asp Gly Tyr Asn Tyr Leu Asp Tyr Ser Ala Asp Leu Phe Gln Ala			
5	255	260	265	
	atc aca gat cat tac gtc cag gtc ctc aac tgt aag cag aac tgt gtc			866
	Ile Thr Asp His Tyr Val Gln Val Leu Asn Cys Lys Gln Asn Cys Val			
	270	275	280	285
10	acg gag ctg gct tcc cac cca agt agg gaa aag ccc ttt gaa gac ttc			914
	Thr Glu Leu Ala Ser His Pro Ser Arg Glu Lys Pro Phe Glu Asp Phe			
	290	295	300	
15	ctc cct tca cac tat aat tac cta cag ttt gcc tac tac aac att ggg			962
	Leu Pro Ser His Tyr Asn Tyr Leu Gln Phe Ala Tyr Tyr Asn Ile Gly			
	305	310	315	
	aac tat aca caa gct att gaa tgt gcc aag acc tac ctc ctc ttc ttt			1010
20	Asn Tyr Thr Gln Ala Ile Glu Cys Ala Lys Thr Tyr Leu Leu Phe Phe			
	320	325	330	
	ccc aat gat gag gtg atg cac cag aat ctg gct tat tac aca gcc atg			1058
	Pro Asn Asp Glu Val Met His Gln Asn Leu Ala Tyr Tyr Thr Ala Met			
25	335	340	345	
	ctt gga gaa gaa gag gcc agc tcc atc agc ccc agg gag aat gcc gag			1106
	Leu Gly Glu Glu Glu Ala Ser Ser Ile Ser Pro Arg Glu Asn Ala Glu			
	350	355	360	365
30	gaa tac cga cgt cca aac ctg ttg gag aaa gaa ctg ctt ttc ttc gct			1154
	Glu Tyr Arg Arg Pro Asn Leu Leu Glu Lys Glu Leu Leu Phe Phe Ala			
	370	375	380	
35	tat gac att ttt gga att ccc ttt gtg gat ccc gat tca tgg act cca			1202
	Tyr Asp Ile Phe Gly Ile Pro Phe Val Asp Pro Asp Ser Trp Thr Pro			

[illegible]

530

535

540

caa tagaagagtc acaggctgag aggaaggaca gtagccaccc cgtccacgtg 1687

Gln

5

gataactgca tcctgaatgc cgaagccttc atgtgtatca aggagccccc agcatacacg 1747

ttccgggaat acagcgccat cctttacctc aatggcgact tcgatggagg aaactttttac 1807

10 ttcacagaac tagatgccaa gactgtgacg gcagaggtgc agccccagtg tggaagggtc 1867

gtgggattct cttctggcac tgagaacca catggagtga aggctgtcac cagggggcag 1927

cgctgcgcca tcgccctgtg gttcacgtg gatcctcggc acagtgagag agacagggtg 1987

15

caggcagatg acctggtgaa gatgctgttc agcccagaag aggtggacct cccccaggaa 2047

cagccccctgc ctgaccagca gggttcgcca gagcctggag aagagtttct gcatggtgct 2107

20 actgttcttg gagtgggcat agcaggacac actcttctct gggcttggct gtaggctcag 2167

aatgcaggcc cagaaccacc ctggggccta ttaggcagc tgccgtcagc agcgtgatat 2227

atttaagtgt ctgtaaagac aaccaaagaa taaatgattt gtgtttttta aaagnaaaaa 2287

25

aaaaaaaaa ttaaaaattt gcgcggccgc aagaa 2322

<210> 8

30 <211> 542

<212> PRT

<213> Mus musculus

<400> 8

35 Met Ala Val Thr Lys Gly Gly Cys Trp His Asp Ala Ser Gly Arg Arg

1

5

10

15

	Arg Arg Arg Leu Thr Gly Cys Gly Glu Ser Glu Pro Gly Trp Asp Val	
	20	25 30
5	Ala Ala Pro Asp Leu Leu Tyr Ala Glu Gly Thr Ala Ala Tyr Ser Arg	
	35	40 45
	Arg Asp Trp Pro Gly Val Val Leu Asn Met Glu Arg Ala Leu Arg Ser	
	50	55 60
10	Arg Ala Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Arg Cys Ala	
	65	70 75 80
	Thr Glu Leu Pro Trp Ala Pro Asp Leu Asp Leu Gly Pro Asp Pro Ser	
15		85 90 95
	Leu Ser Gln Asp Pro Gly Ala Ala Ala Leu His Asp Leu Arg Phe Phe	
	100	105 110
20	Gly Ala Val Leu Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro	
	115	120 125
	Pro Ser Ala His Leu Leu Ser Glu Glu Leu Asp Leu Glu Phe Asn Lys	
	130	135 140
25	Arg Ser Pro Tyr Asn Tyr Leu Gln Val Ala Tyr Phe Lys Ile Asn Lys	
	145	150 155 160
	Leu Glu Lys Ala Val Ala Ala Ala His Thr Phe Phe Val Gly Asn Pro	
30		165 170 175
	Glu His Met Glu Met Arg Gln Asn Leu Asp Tyr Tyr Gln Thr Met Ser	
	180	185 190
35	Gly Val Lys Glu Ala Asp Phe Arg Asp Leu Glu Ala Lys Pro His Met	
	195	200 205

	His	Glu	Phe	Arg	Leu	Gly	Val	Arg	Leu	Tyr	Ser	Glu	Glu	Lys	Pro	Gln	
	210						215					220					
5	Glu	Ala	Val	Pro	His	Leu	Glu	Ala	Ala	Leu	Gln	Glu	Tyr	Phe	Val	Ala	
	225					230					235					240	
	Asp	Glu	Glu	Cys	Arg	Ala	Leu	Cys	Glu	Gly	Pro	Tyr	Asp	Tyr	Asp	Gly	
					245					250						255	
10	Tyr	Asn	Tyr	Leu	Asp	Tyr	Ser	Ala	Asp	Leu	Phe	Gln	Ala	Ile	Thr	Asp	
				260						265						270	
	His	Tyr	Val	Gln	Val	Leu	Asn	Cys	Lys	Gln	Asn	Cys	Val	Thr	Glu	Leu	
15			275					280							285		
	Ala	Ser	His	Pro	Ser	Arg	Glu	Lys	Pro	Phe	Glu	Asp	Phe	Leu	Pro	Ser	
			290					295							300		
20	His	Tyr	Asn	Tyr	Leu	Gln	Phe	Ala	Tyr	Tyr	Asn	Ile	Gly	Asn	Tyr	Thr	
	305					310					315					320	
	Gln	Ala	Ile	Glu	Cys	Ala	Lys	Thr	Tyr	Leu	Leu	Phe	Phe	Pro	Asn	Asp	
					325						330					335	
25	Glu	Val	Met	His	Gln	Asn	Leu	Ala	Tyr	Tyr	Thr	Ala	Met	Leu	Gly	Glu	
				340							345					350	
	Glu	Glu	Ala	Ser	Ser	Ile	Ser	Pro	Arg	Glu	Asn	Ala	Glu	Glu	Tyr	Arg	
30			355					360						365			
	Arg	Pro	Asn	Leu	Leu	Glu	Lys	Glu	Leu	Leu	Phe	Phe	Ala	Tyr	Asp	Ile	
			370					375						380			
35	Phe	Gly	Ile	Pro	Phe	Val	Asp	Pro	Asp	Ser	Trp	Thr	Pro	Glu	Glu	Val	
	385					390					395					400	

Ile Pro Lys Arg Leu Gln Glu Lys Gln Lys Ser Glu Arg Glu Thr Ala
 405 410 415

5 Val Arg Ile Ser Gln Glu Ile Gly Asn Leu Met Lys Glu Ile Glu Thr
 420 425 430

Leu Val Glu Glu Lys Thr Lys Glu Ser Leu Asp Val Ser Arg Leu Thr
 435 440 445

10 Arg Glu Gly Gly Pro Leu Leu Tyr Glu Gly Ile Ser Leu Thr Met Asn
 450 455 460

Ser Lys Val Leu Asn Gly Ser Gln Arg Val Val Met Asp Gly Val Ile
 15 465 470 475 480

Ser Asp Asp Glu Cys Gln Glu Leu Gln Arg Leu Thr Asn Ala Ala Ala
 485 490 495

20 Thr Ser Gly Asp Gly Tyr Arg Gly Gln Thr Ser Pro His Thr Pro Asn
 500 505 510

Glu Lys Phe Tyr Gly Val Thr Val Leu Lys Ala Leu Lys Leu Gly Gln
 515 520 525

25 Glu Gly Lys Val Pro Leu Gln Ser Ala Arg Thr Ala Leu Gln
 530 535 540

30 <210> 9
 <211> 28
 <212> DNA
 <213> Artificial Sequence

35 <220>
 <223> Description of Artificial Sequence: Artificially

Synthesized Primer Sequence

	<400> 9	
	ggatccaagg agcgggctct gcgctcgc	19
5		
	<210> 10	
	<211> 21	
	<212> DNA	
10	<213> Artificial Sequence	
	<220>	
	<223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence	
15		
	<400> 10	
	ccaagcttgg ctgtgtaata a	21
20	<210> 11	
	<211> 19	
	<212> DNA	
	<213> Artificial Sequence	
25	<220>	
	<223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence	
	<400> 11	
30	tcattacatc caggtcctc	19
	<210> 12	
	<211> 20	
35	<212> DNA	
	<213> Artificial Sequence	

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

5

<400> 12

tttggagttc atggtgagac

20

10 <210> 13

<211> 38

<212> DNA

<213> Artificial Sequence

15 <220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 13

20 agatctagat ctatggcggc acgcgcgttg aagctgct

38

<210> 14

<211> 39

25 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

30

<400> 14

gtcgacgtcg acttcatagc tcatccttgg gcttcgatt

39

35

<210> 15

<211> 40

<212> DNA

<213> Artificial Sequence

5 <220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 15

10 gtcgacgtcg actctaggtg ccctgctcac gggggccgat

40

[Brief Description of the Drawings]

[Fig. 1]

15 Fig. 1 shows the alignments for the mouse Gros1 sequence and
the EST sequence.

[Fig. 2]

Fig. 2 shows the splicing form for cDNA of mouse Gros1.

[Fig. 3]

Fig. 3 shows the splicing form for cDNA of human Gros1.

20 [Fig. 4]

Fig. 4 shows the result of Northern analysis in mouse tissues
using the mouse Gros1 cDNA probe.

[Fig. 5]

25 Fig. 5 shows the result of Northern analysis in human cells
using the mouse Gros1 cDNA probe.

[Fig. 6]

Fig. 6 shows the result of Northern analysis in human tissues
using the mouse Gros1 cDNA probe.

[Fig. 7]

30 Fig. 7 shows the result of Western analysis for human GFP-Gros1L
and GFP-Gros1S expressed in COS7.

[Fig. 8]

Fig. 8 shows localization of human GFP-Gros1L and human
GFP-Gros1S in cells.

35 [Fig. 9]

Fig. 9 shows the result of Northern analysis in NIH3T3 cells

to which mouse Gros1L, Gros1 mutant and Gros1 antisense were introduced.

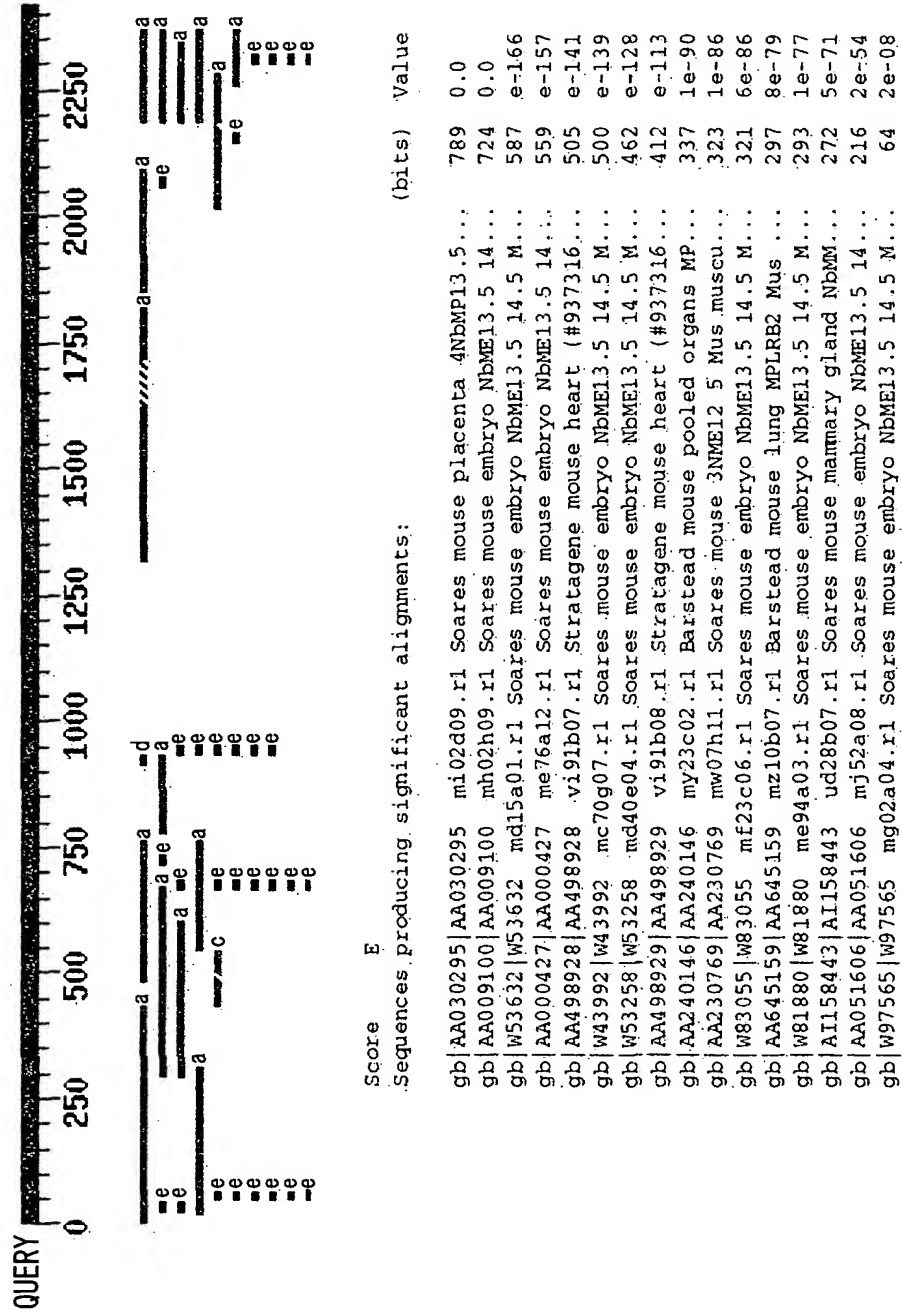
[Fig. 10]

Fig. 10 shows the result of analysis of colony forming activity
5 of NIH3T3 cells to which mouse Gros1L, Gros1 mutant and Gros1 antisense
were introduced.

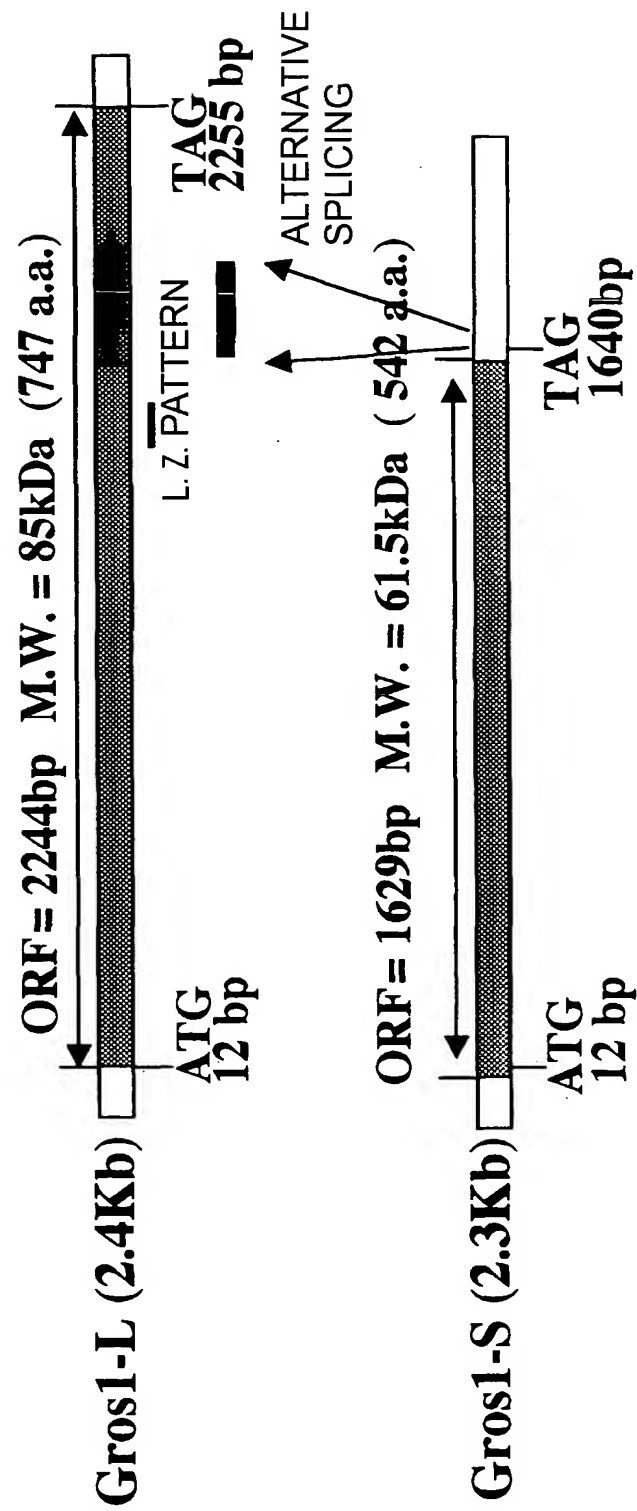
[Document Name] DRAWINGS

[Fig. 1]

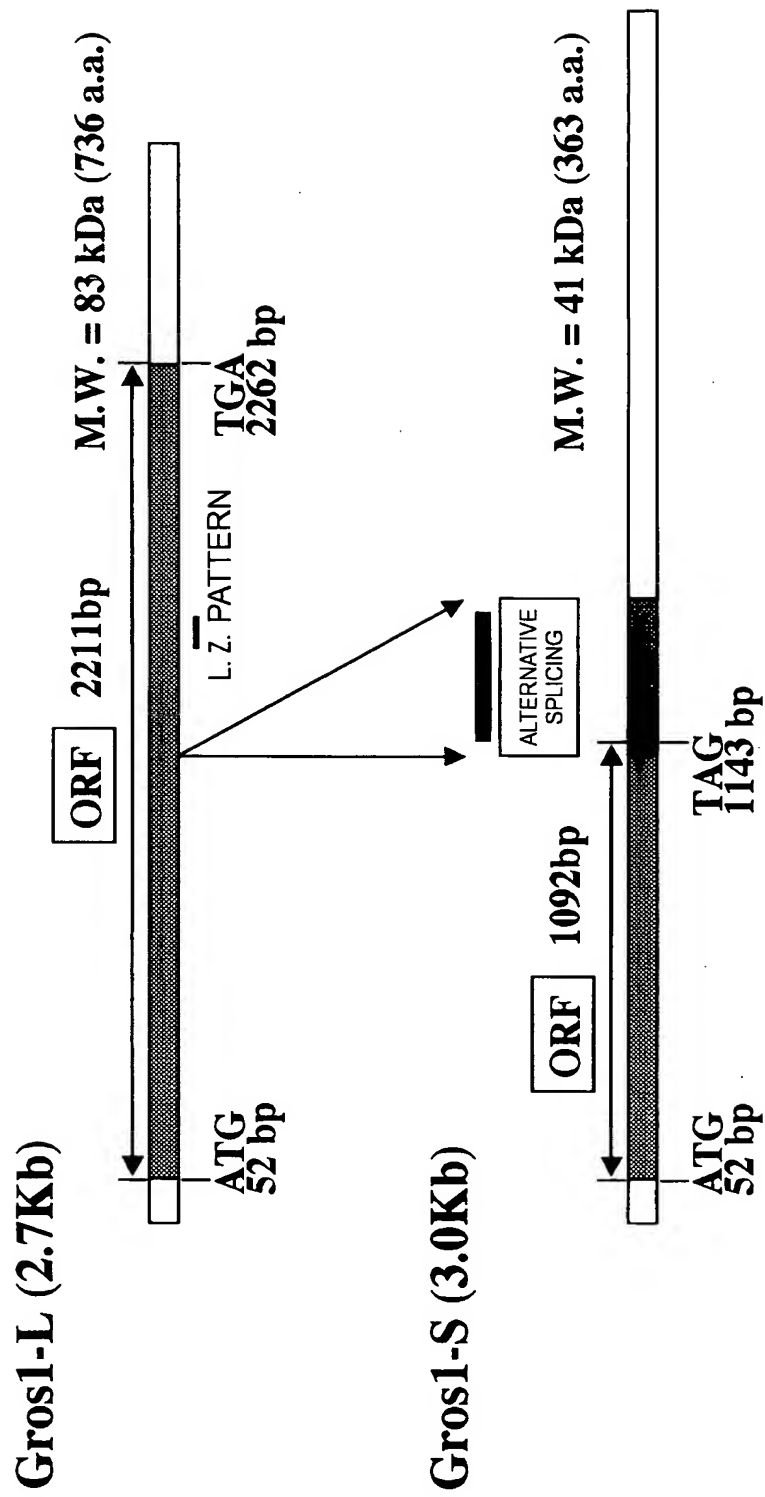
MOUSE #7 ESTS

ALIGNMENT SCORE a: ≥ 200 , b: 80-200, c: 50-80, d: 40-50, e: < 40 

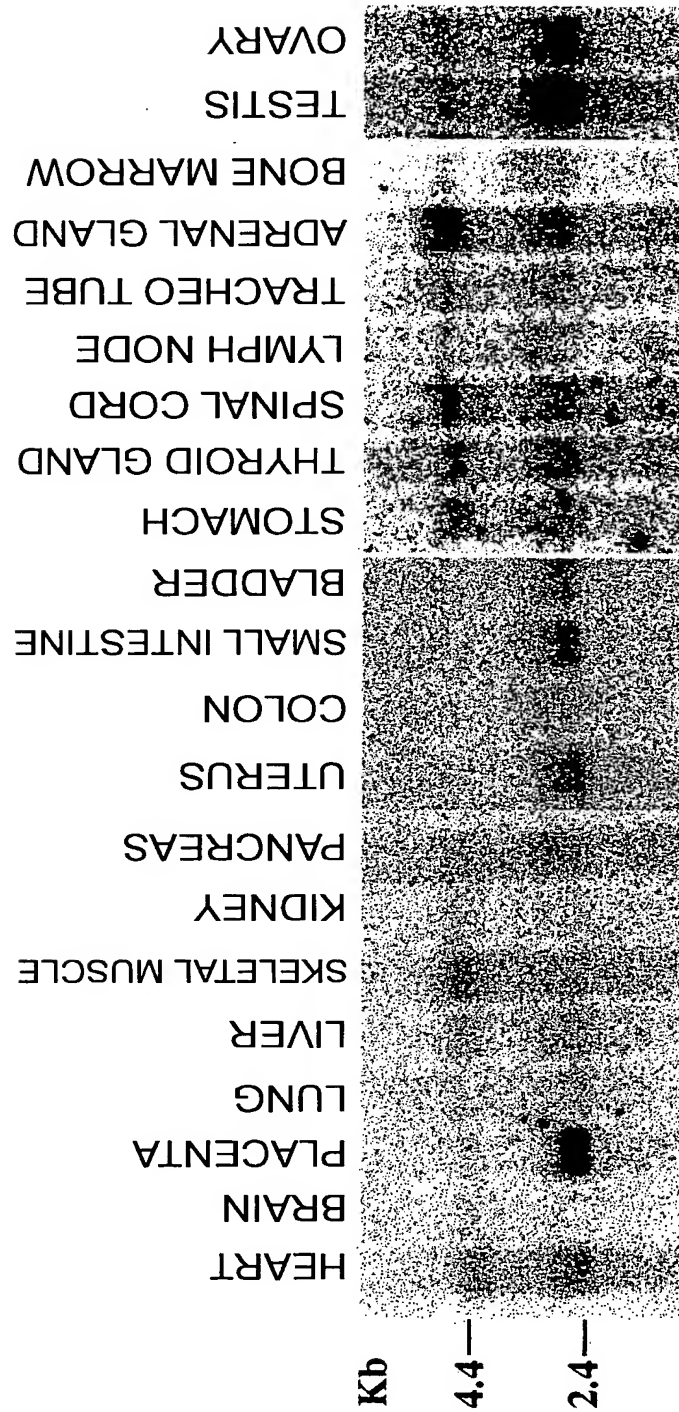
[Fig. 2]



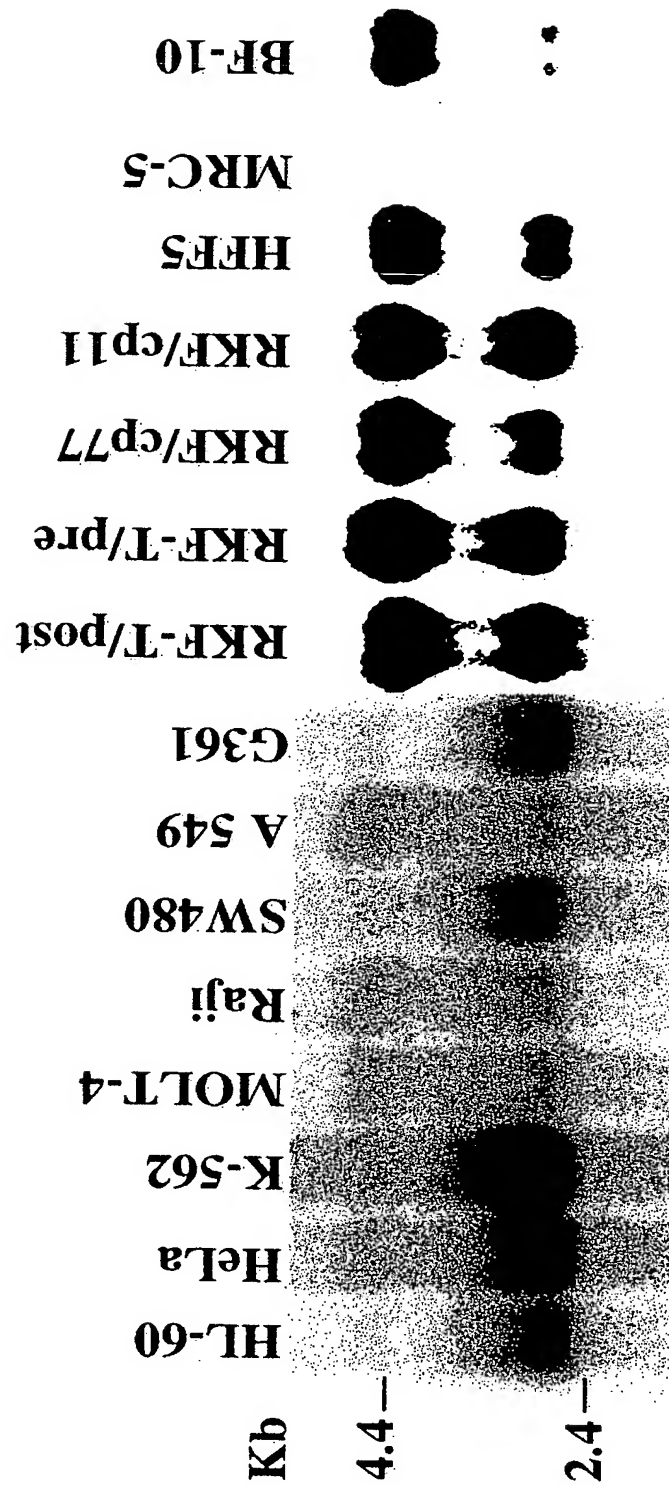
[Fig. 3]



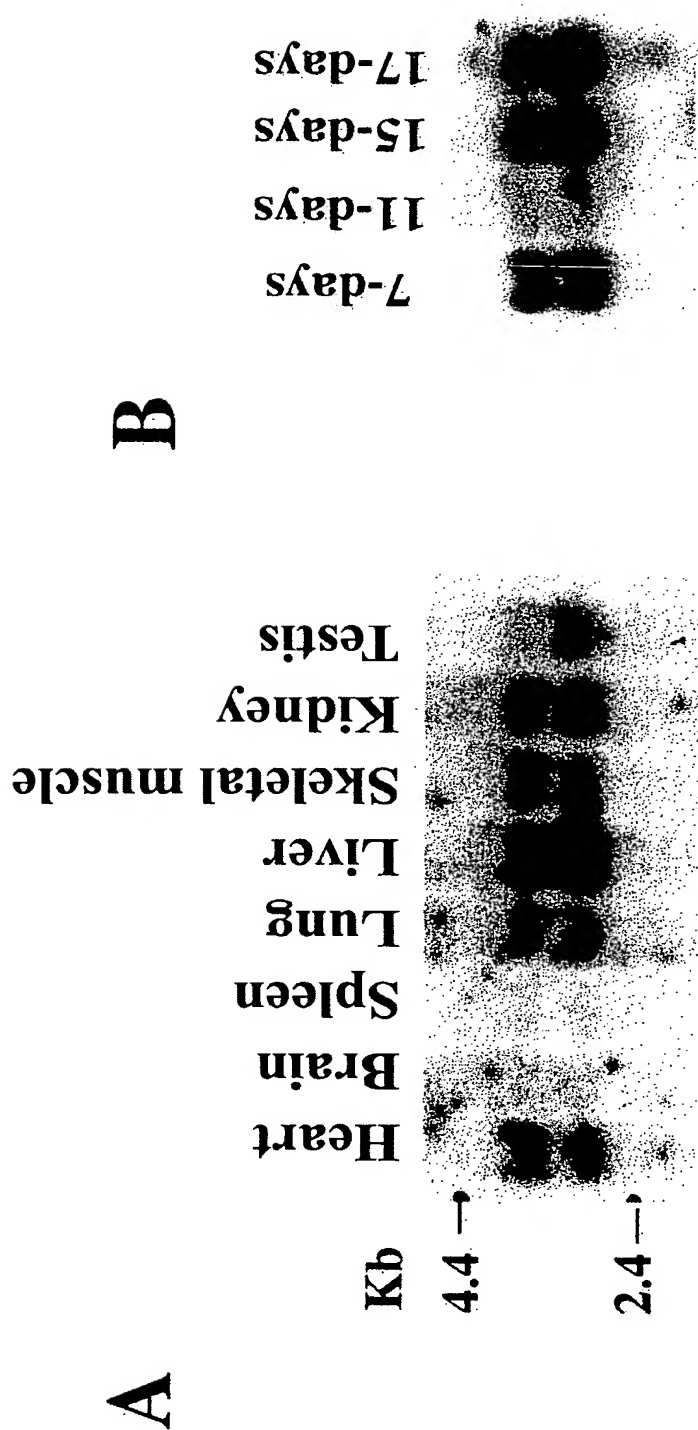
[Fig. 4]



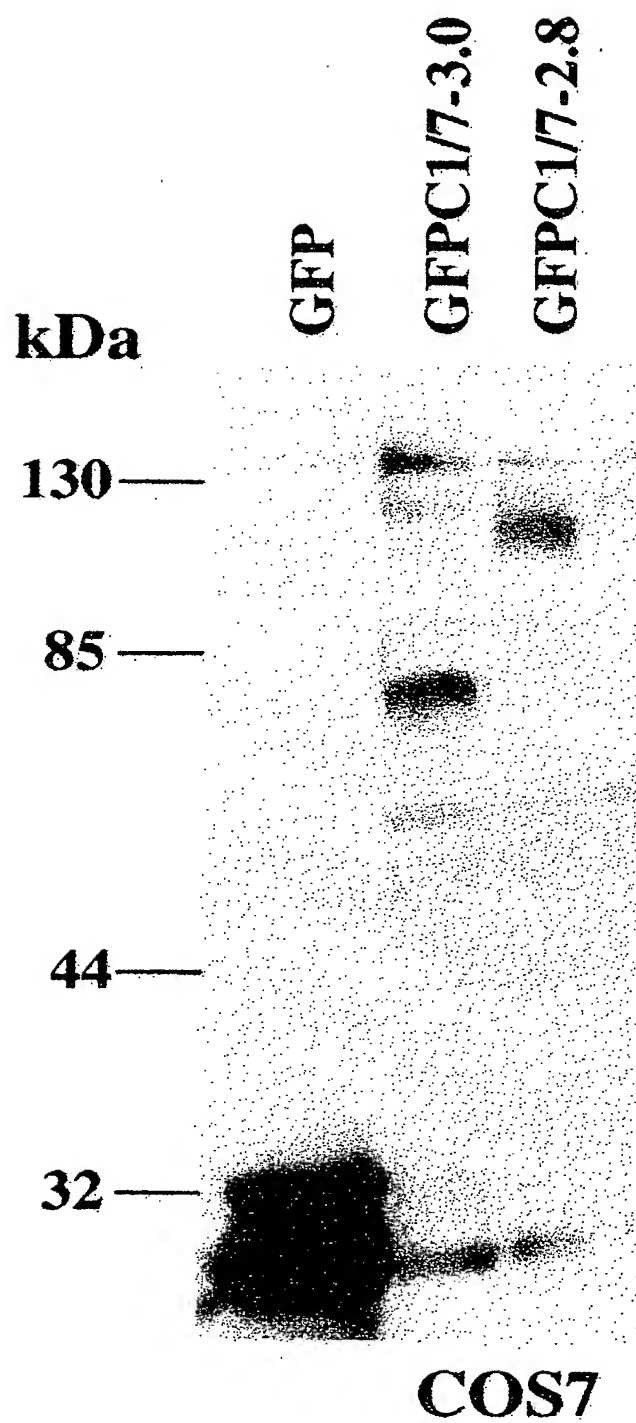
[Fig. 5]



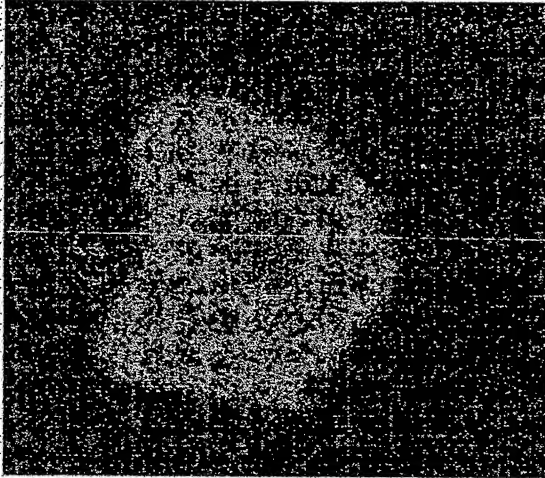
[Fig. 6]



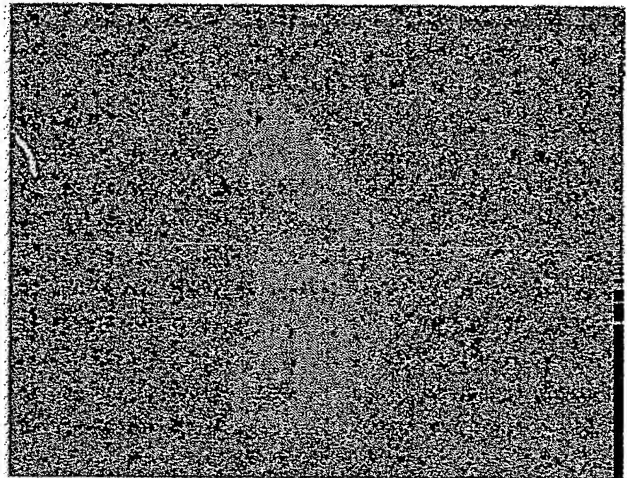
[Fig. 7]



[Fig. 8]

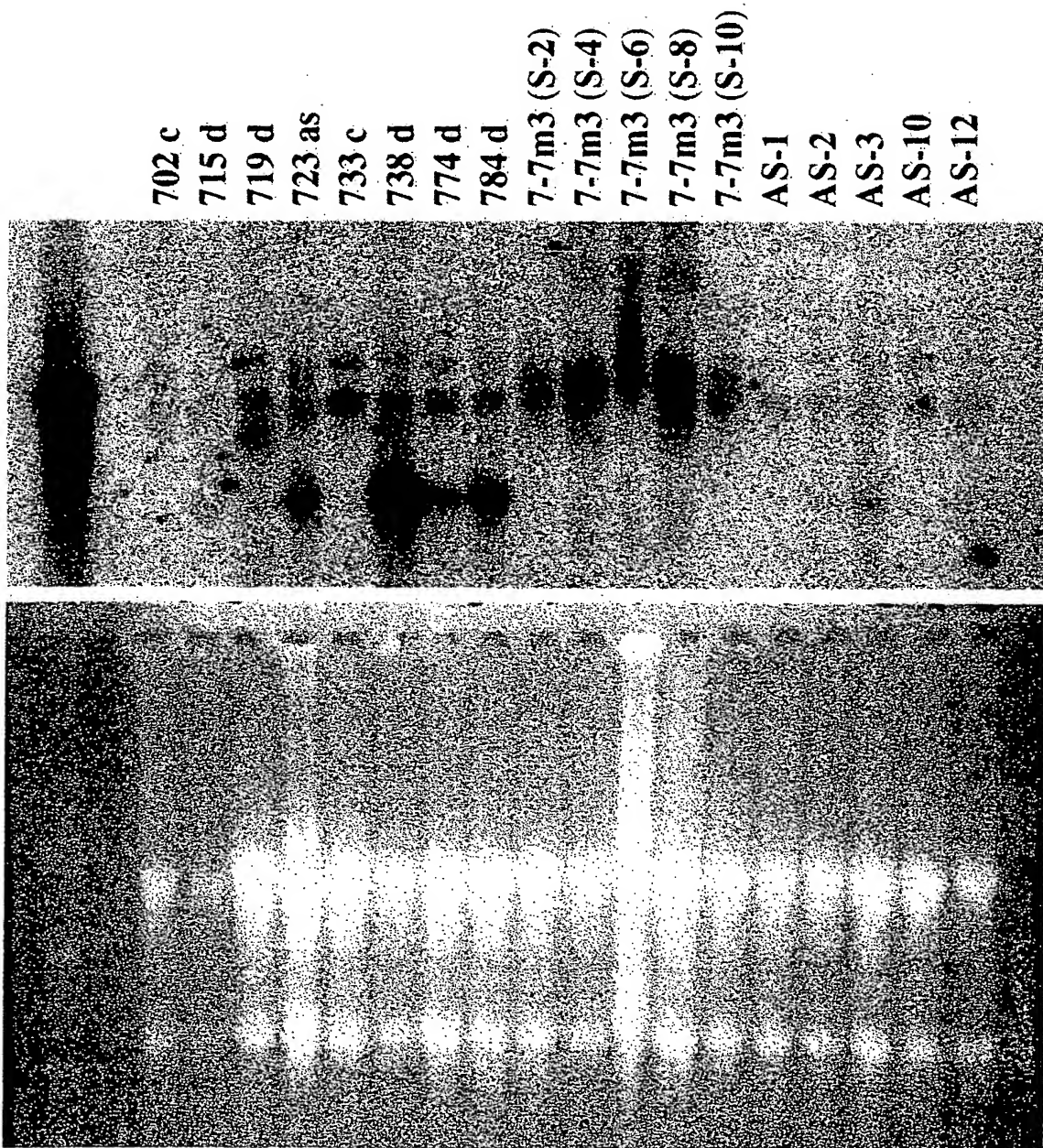


GFPC1/7:2.8kb (83 kDa)

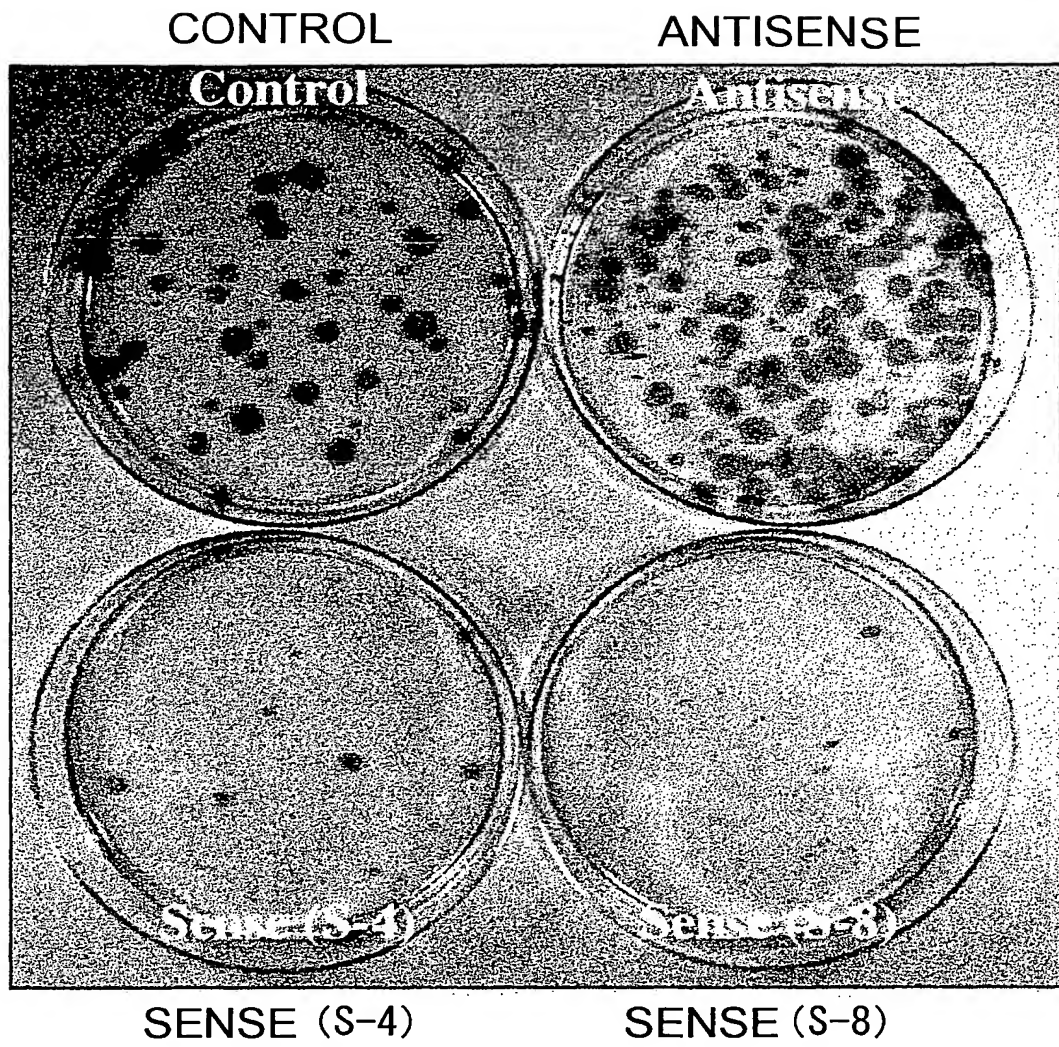


GFPC1/7:3.0 kb (41 kDa)

[Fig. 9]



[Fig. 10]



[Document Name] ABSTRACT

[Abstract]

[Problems to Be Solved] The object of the present invention is to provide a novel protein involved in the control of cell proliferation and a gene thereof, as well as methods for producing and using the same.

[Means to Solve the Problems] A full-length cDNA encoding novel proteins involved in the control of cell proliferation (human Gros1-L and S) was successfully isolated from the human testis cDNA libraries.

A full-length cDNA encoding the mouse homologues of the human Gros1 (mouse Gros1-L and S) was also isolated. The colony forming activity of cells exogenously expressing Gros1-L was significantly reduced, while that of cells expressing Gros1 antisense RNA was significantly increased.

[Selected Drawings] None

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.